

## 2) INFORMATION FOR SEQ ID NO: 2117

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117

GCGGGCGACG CCATTGAGCC ACCTTCGAGA GCCCGC

36

## 2) INFORMATION FOR SEQ ID NO: 2118

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118

GCGGGCTCCT TGACAATTTC TTCGTATCTG TTCTTGGCCC GC

42

## 2) INFORMATION FOR SEQ ID NO: 2119

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119

GCGGGCTTAC AACCTAAGG CTGTTCCATT CGTTGCCCGC

40

## 2) INFORMATION FOR SEQ ID NO: 2120

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120

GCAGGGCAGAA ACCAAGGCTG GTAAGGTTAC CGGTAGCCCCG C

41

2) INFORMATION FOR SEQ ID NO: 2121

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121

CGACCGCIAG CCGCACACCA AGTTCCGGTC G

31

2) INFORMATION FOR SEQ ID NO: 2122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122

CCGAGCGAAT GTAGGAGTCC AGGGTCTCTG CTCGG

35

2) INFORMATION FOR SEQ ID NO: 2123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123

TCTACCACTG AAGCATTAC

19

## 2) INFORMATION FOR SEQ ID NO: 2124

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124

TAGGTACTGT AGGTTTATTG

20

## 2) INFORMATION FOR SEQ ID NO: 2125

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125

CACGCGGATT TTGAATCTCT TCCTCTAGTA GCGCGTG

37

## 2) INFORMATION FOR SEQ ID NO: 2126

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126

ATATCAGAGA CTGATGAG

18

## 2) INFORMATION FOR SEQ ID NO: 2127

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127

TAGCATATTC AGAGAATATT GT

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2) INFORMATION FOR SEQ ID NO: 2128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128

CAACGCTGGA GAATCTATAT TTGTAGAAAC TGCAGTTG

37

2) INFORMATION FOR SEQ ID NO: 2129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8133 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X51797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129

ATGTCTTTAA	TATCTAAAGA	AGAGTTAATA	AAACTCGCAT	ATAGCATTAG	50
ACCAAGAGAA	AATGAGTATA	AAACTATACT	AACTAATTAA	GACGAATATA	100
ATAAGTTAAC	TACAAACAAT	AATGAAAATA	AATATTTGCA	ATTAACAAAAAA	150
CTAAATGAAT	CAATTGATGT	TTTTATGAAT	AAATATAAAA	CTTCAAGCAG	200
AAATAGAGCA	CTCTCTAAC	AAAAAAAGA	TATATTAAAA	GAAGTAATTC	250
TTATTAAAAA	TTCCAATACA	AGCCCTGTAG	AAAAAAATT	ACATTTGTA	300
TGGATAGGTG	GAGAAGTCAG	TGATATTGCT	CTTGAATACA	AAAACAATG	350
GGCTGATATT	AATGCAGAAT	ATAATATTAA	ACTGTGGTAT	GATAGTGAAG	400
CATTCTTAGT	AAATACACTA	AAAAAGGCTA	TAGTTGAATC	TTCTACCACT	450
GAAGCATTAC	AGCTACTAGA	GGAAGAGATT	CAAAATCCTC	AATTTGATAA	500
TATGAAATT	TACAAAAAAA	GGATGGAATT	TATATATGAT	AGACAAAAAA	550
GGTTTATAAA	TTATTATAAA	TCTCAAATCA	ATAAACCTAC	AGTACCTACA	600
ATAGATGATA	TTATAAAGTC	TCATCTAGTA	TCTGAATATA	ATAGAGATGA	650
AACTGTATTA	GAATCATATA	GAACAAATTC	TTTGAGAAAA	ATAAAATAGTA	700
ATCATGGGAT	AGATATCAGG	GCTAATAGTT	TGTTTACAGA	ACAAGAGTTA	750
TTAAATATTT	ATAGTCAGGA	GTTGTTAAAT	CGTGGAAATT	TAGCTGCAGC	800

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ATCTGACATA	GTAAGATTAT	TAGCCCTAAA	AAATTTGGC	GGAGTATATT	850
TAGATGTTGA	TATGCTTCCA	GGTATTCACT	CTGATTTATT	TAAAACAATA	900
TCTAGACCTA	GCTCTATTGG	ACTAGACCCT	TGGGAAATGA	TAAAATTAGA	950
GGCTATTATG	AAAGTATAAAA	AATATATAAA	TAATTATACA	TCAGAAAAC	1000
TTGATAAACT	TGATCAACAA	TTAAAAGATA	ATTTTAAACT	CATTATAGAA	1050
AGTAAAAGTG	AAAAATCTGA	GATATTTCT	AAATTAGAAA	ATTTAAATGT	1100
ATCTGATCTT	GAAATTAAAA	TAGCTTTCGC	TTTAGGCAGT	GTTATAAATC	1150
AAGCCTTGAT	ATCAAAACAA	GGTTCATATC	TTACTAACCT	AGTAATAGAA	1200
CAAGTAAAAA	ATAGATATCA	ATTTTAAAC	CAACACCTA	ACCCAGCCAT	1250
AGAGTCTGAT	AATAACTTCA	CAGATACTAC	AAAATTTT	CATGATTCTAT	1300
TATTTAATT	AGCTACCGCA	GAAAACCTA	TGTTTTTAAC	AAAATAGCA	1350
CCATACTTAC	AAAGTAGGTT	TATGCCAGAA	GCTCGCTCCA	CAATAAGTT	1400
AAGTGGTCCA	GGAGCTTATG	CGTCAGCTTA	CTATGATTTC	ATAAATTTAC	1450
AAGAAAATAC	TATAGAAAAA	ACTTTAAAAG	CATCAGATT	AATAGAATT	1500
AAATTCCCAG	AAAATAATCT	ATCTCAATTG	ACAGAACAAAG	AAATAAATAG	1550
TCTATGGAGC	TTTGATCAAG	CAAGTGCAA	ATATCAATT	GAGAAATATG	1600
TAAGAGATTA	TACTGGTGG	TCTCTTCTG	AAGACAATGG	GGTAGACTTT	1650
AATAAAAATA	CTGCCCTCGA	CAAAAACAT	TTATTAAATA	ATAAAATTCC	1700
ATCAAACAAT	GTAGAAGAAG	CTGGAAGTAA	AAATTATGTT	CATTATATCA	1750
TACAGTTACA	AGGAGATGAT	ATAAGTTATG	AAGCAACATG	CAATTATT	1800
TCTAAAATC	CTAAAATAG	TATTATTATA	CAACGAAATA	TGAATGAAAG	1850
TGCAAAAAGC	TACTTTTAA	GTGATGATGG	AGAATCTATT	TTAGAATTAA	1900
ATAAAATATAG	GATACCTGAA	AGATTTAAA	ATAAGGAAA	AGTAAAAGTA	1950
ACCTTATTG	GACATGGTAA	AGATGAATT	AACACAAAGCG	AATTGCTAG	2000
ATTAAGTGT	GATTCACTT	CCAATGAGAT	AAGTCATTT	TTAGATACCA	2050
TAAAATTAGA	TATATCACCT	AAAATGTAG	AAGTAAACTT	ACTTGGATGT	2100
AATATGTTA	GTTATGATT	TAATGTTGAA	GAAACTTATC	CTGGGAAGTT	2150
GCTATTAAGT	ATTATGGACA	AAATTACTTC	CACTTTACCT	GATGTAATA	2200
AAAATTCTAT	TACTATAGGA	GCAAATCAAT	ATGAAGTAAG	AATTAATAGT	2250
GAGGGAAAGAA	AAGAACTTCT	GGCTCACTCA	GGTAAATGGA	AAATAAAAGA	2300
AGAAGCTATT	ATGAGCGATT	TATCTAGTAA	AGAATACATT	TTTTTGATT	2350
CTATAGATAA	TAAGCTAAA	GCAAAGTCCA	AGAATATTCC	AGGATTAGCA	2400
TCAATATCAG	AAGATATAAA	AACATTATTA	CTTGATGCAA	GTGTTAGTCC	2450
TGATACAAAA	TTTATTTAA	ATAATCTAA	GCTTAATATT	GAATCTTCTA	2500
TTGGGGATTA	CATTTATTAT	AAAAAATTAG	AGCCTGTTAA	AAATATAATT	2550
CACAATTCTA	TAGATGATT	AATAGATGAG	TTCAATCTAC	TTGAAAATGT	2600
ATCTGATGAA	TTATATGAAT	AAAAAAATT	AAATAATCTA	GATGAGAACT	2650
ATTTAATATC	TTTTGAAGAT	ATCTCAAAA	ATAATTCAAC	TTACTCTGTA	2700
AGATTTATTA	ACAAAAGTAA	TGGTGAGTCA	GTTTATGTAG	AAACAGAAA	2750
AGAAATTTTT	TCAAAATATA	GCGAACATAT	TACAAAAGAA	ATAAGTACTA	2800
TAAAGAATAG	TATAATTACA	GATGTTAATG	GTAATTATT	GGATAATATA	2850
CAGTTAGATC	ATACTTCTCA	AGTTAATACA	TTAAACCGCAG	CATTCTTAT	2900
TCAATCATTA	ATAGATTATA	GTAGCAATAA	AGATGTACTG	AATGATTAA	2950
GTACCTCAGT	TAAGGTTCAA	CTTTATGCTC	AACTATTAG	TACAGGTTA	3000
AATACTATAT	ATGACTCTAT	CCAATTAGTA	AATTAAATAT	CAAATGCAGT	3050
AAATGATACT	ATAAAATGTAC	TACCTACAAT	AACAGAGGGG	ATACCTATTG	3100
TATCTACTAT	ATTAGACGGA	ATAAACTTAG	GTGCAGCAAT	TAAGGAATT	3150
CTAGACGAAC	ATGACCCATT	ACTAAAAAAA	GAATTAGAAG	CTAAGGTGGG	3200
TGTTTAGCA	ATAAAATATGT	CATTATCTAT	AGCTGCAACT	GTAGCTTCAA	3250
TTGTTGGAAT	AGGTGCTGAA	GTTACTATT	TCTTATTACC	TATAGCTGGT	3300
ATATCTGCAG	GAATACCTTC	ATTAGTTAAT	AATGAATTAA	TATTGCATGA	3350
TAAGGCAACT	TCAGTGGTAA	ACTATTTAA	TCATTGCT	GAATCTAAA	3400
AATATGGCCC	TCTTAAAACA	GAAGATGATA	AAATTAGT	TCCTATTGAT	3450
GATTTAGTAA	TATCAGAAAT	AGATTTAAT	AATAATTGCA	AAAACACTAGG	3500
AACATGTAAT	ATATTAGCAA	TGGAGGGGG	ATCAGGACAC	ACAGTGAETG	3550
GTAATATAGA	TCACCTTTTC	TCATCTCCAT	CTATAAGTTC	TCATATTCT	3600
TCATTATCAA	TTTATTCTGC	AATAGGTATA	GAAACAGAAA	ATCTAGATT	3650

TTCAAAAAAA	ATAATGATGT	TACCTAATGC	TCCTTCAAGA	GTGTTTGGT	3700
GGGAAACTGG	AGCAGTCCA	GGTTTAAGAT	CATTGGAAAA	TGACGGAACT	3750
AGATTACTTG	ATTCAATAAG	AGATTATAC	CCAGGTAAAT	TTTACTGGAG	3800
ATTCTATGCT	TTTTCGATT	ATGCAATAAC	TACATTAAAA	CCAGTTTATG	3850
AAGACACTAA	TATTAACATT	AAACTAGATA	AAGATACTAG	AAACTTCATA	3900
ATGCCAACTA	TAACTACTAA	CGAAATTAGA	AACAAATTAT	CTTATTCAATT	3950
TGATGGAGCA	GGAGGAACCT	ACTCTTATT	ATTATCTTCA	TATCCAATAT	4000
CAACGAATAT	AAATTTATCT	AAAGATGATT	TATGGATATT	TAATATTGAT	4050
AATGAAGTAA	GAGAAATATC	TATAGAAAAT	GGTACTATTA	AAAAAGGAAA	4100
GTAAATAAAA	GATGTTTAA	GTAAAATTGA	TATAAATAAA	AATAAACTTA	4150
TTATAGGCAA	TCAAACAATA	GATTTTCAG	GCGATATAGA	TAATAAAGAT	4200
AGATATATAT	TCTTGACTTG	TGAGTTAGAT	GATAAAATTA	GTTAATAAT	4250
AGAAATAAAT	CTTGTGCAA	AATCTTATAG	TTTGTATTG	TCTGGGGATA	4300
AAAATTATTT	GATATCCAAT	TTATCTAATA	CTATTGAGAA	AATCAAACT	4350
TTAGGCCTAG	ATAGTAAAAA	TATAGCGTAC	AATTACACTG	ATGAATCTAA	4400
TAATAAATAT	TTGGAGCTA	TATCTAAAC	AAGTCAAAAA	AGCATAATAC	4450
ATTATAAAAA	AGACAGTAAA	AATATATTAG	AATTTTATAA	TGACAGTACA	4500
TTAGAATTAA	ACAGTAAAGA	TTTATTGCT	GAAGATATAA	ATGTTATTAT	4550
GAAAGATGAT	ATTAATACTA	TAACAGGAAA	ATACTATGTT	GATAATAATA	5000
CTGATAAAAG	TATAGATTTC	TCTATTCTT	TAGTTAGTAA	AAATCAAGTA	5050
AAAGTAAATG	GATTATATT	AAATGAATCC	GTATACTCAT	CTTACCTTGA	5100
TTTGTGAAA	AATTCAGATG	GACACCATAA	TACTTCTAAT	TTTATGAATT	5150
TATTTTGG	CAATATAAGT	TTCTGGAAAT	TGTTGGGTT	TGAAAATATA	5200
AATTTTGTAA	TCGATAAAATA	CTTTACCCCT	GTTGGTAAA	CTAATCTTGG	5250
ATATGTAGAA	TTTATTGTTG	ACAATAATAA	AAATATAGAT	ATATATTTG	5300
GTGAATGGAA	AACATCGTCA	TCTAAAAGCA	CTATATTTAG	CGGAAATGGT	5350
AGAAATGTTG	TAGTAGAGCC	TATATATAAT	CCTGATACGG	GTGAAGATAT	5400
ATCTACTTCA	CTAGATTTT	CCTATGAACC	TCTCTATGGA	ATAGATAGAT	5450
ATATAAATAA	AGTATTGATA	GCACCTGATT	TATATACAAG	TTAATAAAT	5500
ATTAATACCA	ATTATTATTC	AAATGAGTAC	TACCCCTGAGA	TTATAGTTCT	5550
TAACCCAAAT	ACATTCCACA	AAAAAGTAAA	TATAAATTAA	GATAGTTCTT	5600
CTTTTGAGTA	TAATGGTCT	ACAGAAGGAA	GTGACTTTAT	TTAGTTAGA	5650
TACTTAAAG	AAAGTAATAA	AAAAATATTA	CAAAAAATAA	GAATCAAAGG	5700
TATCTTATCT	AAACTCTAAT	CATTTAATAA	AATGAGTATA	GATTTTAAAG	5750
ATATTAAAAA	ACTATCATT	GGATATATAA	TGAGTAATT	TAAATCATTT	5800
AATTCTGAAA	ATGAATTAGA	TAGAGATCAT	TTAGGATT	AAATAATAGA	5850
TAATAAAACT	TATTACTATG	ATGAAGATAG	TAAATTAGTT	AAAGGATTAA	5900
GCAAGTAATT	GACAATAATA	AGTATTATTT	CAATCCTGAC	ACTGCTATCA	5950
TCTCAAAAGG	TTGGCAGACT	GTAAATGGTA	GTAGATACTA	CTTGATACT	6000
GATACCGCTA	TTGCCTTAA	TGGTTATAAA	ACTATTGATG	GTAAACACTT	6050
TTATTTGAT	AGTGATTGTG	TAGTAAAAAT	AGGTGTGTT	AGTACCTCTA	6100
ATGGATTGAA	ATATTTGCA	CCTGCTAATA	CTTATAATAA	TAACATAGAA	6150
GGTCAGGCTA	TAGTTTATCA	AAGTAAATT	TTAACCTTGA	ATGGTAAAAA	6200
ATATTACTTT	GATAATAACT	CAAAAGCAGT	TACCGGATTG	CAAACATTG	6250
ATAGTAAAAA	ATATTACTTT	AATACTAAC	CTGCTGAAGC	AGCTACTGGA	6300
TGGCAAAC	TTGATGGTAA	AAAATATTAC	TTAACCTA	ACACTGCTGA	6350
AGCAGCTACT	GGATGGCAA	CTATTGATGG	TAAAAAATAT	TACTTTAATA	6400
CTAACACTGC	TATAGCTTCA	ACTGGTTATA	CAATTATTAA	TGGTAAACAT	6450
TTTTATTTA	ATACTGATGG	TATTATGCAG	ATAGGAGTGT	TTAAAGGACC	6500
TAATGGATT	GAATATTTG	CACCTGCTAA	TACGGATGCT	AAACACATAG	6550
AAGGTCAAGC	TATACTTAC	CAAAATGAAT	TCTTAAC	GAATGGTAA	6600
AAATATTACT	TTGGTAGTGA	CTAAAAGCA	GTTACTGGAT	GGAGAATTAT	6650
TAACAATAAG	AAATATTACT	TTAACCTAA	TAATGCTATT	GCTGCAATT	6700
ATCTATGCAC	TATAAATAAT	GACAAGTATT	ACTTTAGTTA	TGATGGAATT	6750
CTTCAAAATG	GATATTAC	TATTGAAAGA	ATAATTCT	ATTTGATGC	6800
TAATAATGAA	TCTAAATGG	TAACAGGAGT	ATTTAAAGGA	CCTAATGGAT	6850
TTGAGTATT	TGCACCTGCT	AATACTCACA	ATAATAACAT	AGAAGGTCA	6900

GCTATAGTTT	ACAGAACAA	ATTCTTAAC	TTGAATGGCA	AAAAATATTA	6950
TTTGATAAT	GACTCAAAAG	CAGTTACTGG	ATGGCAAACC	ATTGATGGTA	7000
AAAAATATTA	CTTTAATCTT	AACACTGCTG	AAGCAGCTAC	TGGATGGCAA	7050
ACTATTGATG	GTAAAAAATA	TTACTTTAAT	CTTAACACTG	CTGAAGCAGC	7100
TACTGGATGG	CAAACATTG	ATGGTAAAAA	ATATTACTTT	AATACTAAC	7150
CTTTCATAGC	CTCAACTGGT	TATACAAGTA	TTAATGGTAA	ACATTTTAT	7200
TTTAATACTG	ATGGTATTAT	GCAGATAGGA	GTGTTAAAG	GACCTAATGG	7250
ATTGAAATAC	TTGACACTG	CTAATACCGA	TGCTAACAAAC	ATAGAAGGTC	7300
AAGCTATACT	TTACCAAAAT	AAATTCTAA	CTTGATGG	TAAAAAATAT	7350
TACTTTGGTA	GTGACTCAAA	AGCAGTTACC	GGACTGCGAA	CTATTGATGG	7400
TAAAAAATAT	TACTTTAATA	CTAACACTGC	TGTTGCAGTT	ACTGGATGGC	7450
AAACTATTAA	TGGTAAAAAA	TACTACTTA	ATACTAACAC	TTCTATAGCT	7500
TCAACTGGTT	ATACAATTAT	TAGTGGTAAA	CATTTTTATT	TTAATACTGA	7550
TGGTATTATG	CAGATAGGAG	TGTTTAAAGG	ACCTGATGGA	TTTGAATACT	7600
TTGCACCTGC	TAATACAGAT	GCTAACAAATA	TAGAAGGTCA	AGCTATACGT	7650
TATCAAAATA	GATTCTATA	TTTACATGAC	AATATATATT	ATTTGGTAA	7700
TAATTCAAAA	GCGGCTACTG	GTTGGGTAAC	TATTGATGGT	AATAGATATT	7750
ACTTCGAGCC	TAATACAGCT	ATGGGTGCGA	ATGGTTATAA	AACTATTGAT	7800
AATAAAAATT	TTTACTTTAG	AAATGGTTA	CCTCAGATAG	GAGTGTAA	7850
AGGGTCTAAT	GGATTTGAAT	ACTTTGCACC	TGCTAACACG	GATGCTAAC	7900
ATATAGAAGG	TCAAGCTATA	CGTTATCAA	ATAGATTCT	ACATTTACTT	7950
GGAAAAAATAT	ATTACTTTGG	TAATAATTCA	AAAGCAGTTA	CTGGATGGCA	8000
AACTATTAAT	GGTAAAGTAT	ATTACTTTAT	GCCTGATACT	GCTATGGCTG	8050
CAGCTGGTGG	ACTTTTCGAG	ATTGATGGT	TTATATATTT	CTTGGTGT	8100
GATGGAGTAA	AAGCCCTGG	GATATATGGC	TAA		8133

## 2) INFORMATION FOR SEQ ID NO: 2130

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: VPI 10463
- (C) ACCESSION NUMBER: X53138

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130

ATGAGTTTAG	TTAATAGAAA	ACAGTTAGAA	AAAATGGCAA	ATGTAAGATT	50
TCGTACTCAA	GAAGATGAAT	ATGTTGCAAT	ATTGGATGCT	TTAGAAGAAT	100
ATCATAATAT	GTCAGAGAAT	ACTGTAGTCG	AAAATATTT	AAAATTA	150
GATATAAATA	GTTAACAGA	TATTTATATA	GATACATATA	AAAATCTGG	200
TAGAAATAAA	GCCTAAAAAA	AATTAGGA	ATATCTAGTT	ACAGAAGTAT	250
TAGAGCTAAA	GAATAATAAT	TTAACCTCAG	TTGAGAAAAAA	TTTACATT	300
GTTTGGATTG	GAGGTCAAAT	AAATGACACT	GCTATTAATT	ATATAATCA	350
ATGGAAAGAT	GTAAATAGT	ATTATAATGT	TAATGTTTT	TATGATAGTA	400
ATGCATTTT	GATAAACACA	TTGAAAAAAA	CTGAGTAGA	ATCAGCAATA	450
AATGATACAC	TTGAATCATT	TAGAGAAAAC	TTAAATGACC	CTAGATTG	500
CTATAATAAA	TTCTTCAGAA	AACGTATGGA	AATAATTAT	GATAAACAGA	550
AAAATTCAT	AAACTACTAT	AAAGCTCAA	GAGAAGAAAA	TCCTGAAC	600

ATAATTGATG	ATATTGTA	AA	GACATATCTT	TC	CAAATGAGT	ATTCAAAGGA	650
GATAGATGAA	CTTAATACCT	ATATTGAA	AG	TCCTTAAAT	AAAATTACAC	700	
AGAATAGTGG	AAATGATGTT	AGAAACTTG	AAGAATTAA	AAATGGAGAG		750	
TCATTCAACT	TATATGAACA	AGAGTTGGT	GAAAGGTGGA	ATTTAGCTGC		800	
TGCTTCTGAC	ATATTAAGAA	TATCTGCATT	AAAAGAAATT	GGTGGTATGT		850	
ATTTAGATGT	TGATATGTT	CCAGGAATAC	AACCAGACTT	ATTTGAGTCT		900	
ATAGAGAAAC	CTAGTTCA	GT	AACAGTGGAT	TTTGGAAA	TGACAAAGTT	950	
AGAAGCTATA	ATGAAATACA	AGAAATATAT	ACCAGAATAT	ACCTCAGAAC		1000	
ATTTGACAT	GTTAGACGAA	GAAGTCA	GTAGTTTG	ATCTGTTCTA		1050	
GCTTCTAAGT	CAGATAAAC	AGAAATATTC	TCATCACTTG	GTGATATGGA		1100	
GGCATCACCA	CTAGAAGTT	AAATTGCATT	TAATAGTAAG	GGTATTATAA		1150	
ATCAAGGGCT	AATTTCTGTG	AAAGACTCAT	ATTGTAGCAA	TTTAATAGTA		1200	
AAACAAATCG	AGAATAGATA	AAAATATTG	AATAATAGTT	TAAATCCAGC		1250	
TATTAGCGAG	GATAATGATT	TTAATACTAC	AACGAATACC	TTTATTGATA		1300	
GTATAATGGC	TGAAGCTAAT	GCAGATAATG	GTAGATTTAT	GATGGAAC		1350	
GGAAAGTATT	TAAGAGTTGG	TTCTTCCC	GATGTTAAA	CTACTATTAA		1400	
CTTAAGTGGC	CCTGAAGCAT	ATGCGGCAGC	TTATCAAGAT	TTATTAAATGT		1450	
TTAAAGAAGG	CAGTATGAAT	ATCCATTG	TAGAAGCTGA	TTTAAGAAAC		1500	
TTTGAATCT	CTAAAACAA	TATTCCTCAA	TCAACTGAAC	AAGAAATGGC		1550	
TAGCTTATGG	TCATTGACG	ATGCAAGAGC	TAAAGCTCAA	TTTGAAGAAAT		1600	
ATAAAAGGAA	TTATTTGAA	GGTTCTCTG	GTGAAGATGA	TAATCTTGAT		1650	
TTTTCTCAAA	ATATAGTAGT	TGACAAGGAG	TATCTTTAG	AAAAAAATATC		1700	
TTCATTAGCA	AGAAGTTCA	AGAGAGGATA	TATACACTAT	ATTGTTCA		1750	
TACAAGGAGA	AAAATTAGT	TATGAAGCAG	CATGTAAC	TTTGCAAAAG		1800	
ACTCCTTATG	ATAGTGTACT	GT	TTTCAGAAA	AATATAGAAG	ATTCAAGAAAT	1850	
TGCATATTAT	TATAATCCTG	GAGATGGTGA	AATACAAGAA	ATAGACAAGT		1900	
ATAAAATTCC	AAGTATAATT	TCTGATAGAC	CTAAGATTAA	ATTAACATT		1950	
ATTGGTCATG	GTAAAGATGA	ATTTAATACT	GATATATTG	CAGGTTTG		2000	
TGTAGATTCA	TTATCCACAG	AAATAGAAC	AGCAATAGAT	TTAGCTAAAG		2050	
AGGATATTC	TCCTAAGTCA	ATAGAAATAA	ATTTATTAGG	ATGTAATATG		2100	
TTTAGCTACT	CTATCAACGT	AGAGGAGACT	TATCCTGGAA	AATTATTACT		2150	
TAAAGTTAAA	GATAAAATAT	CAGAATTAA	GCCATCTATA	AGTCAAGACT		2200	
CTATTATAGT	AAAGTCAAAT	CAATATGAAG	TTAGAATAAA	TAGTGAAGGA		2250	
AGAAGAGAAT	TATTGGATCA	TTCTGGTGA	TGGATAAA	AAGAAGAAAG		2300	
TATTATAAAG	GATATTTCAT	CAAAAGAATA	TATATCATTT	AATCCTAAAG		2350	
AAAATAAAAT	TACAGTAAA	TCTAAAATT	TACCTGAGCT	ATCTACATTA		2400	
TTACAAGAAA	TTAGAAATAA	TTCTAATTCA	AGTGATATTG	AACTAGAAGA		2450	
AAAAGTAATG	TTAACAGAAT	GTGAGATAAA	TGTTATTTCA	AATATAGATA		2500	
CGCAAATTGT	TGAGGAAAGG	ATTGAAGAAG	CTAAGAATT	AACTCTGAC		2550	
TCTATTAAATT	ATATAAAAGA	TGAATTAAA	CTAATAGAAT	CTATTTCTGA		2600	
TGCACTATGT	GACTAAAAC	AACAGAATGA	ATTAGAAGAT	TCTCATT		2650	
TATCTTTGA	GGACATATCA	GAGACTGATG	AGGGATTAG	TATAAGATT		2700	
ATTAATAAAG	AAACTGGAGA	ATCTATATT	GTAGAAACTG	AAAAAAACAAT		2750	
ATTCTCTGAA	TATGCTAATC	ATATAACTGA	AGAGATTCT	AAGATAAAAG		2800	
GTACTATATT	TGATACTGTA	AATGGTAAGT	TAGTAAAAAA	AGTAAATT		2850	
GATACTACAC	ACGAAGTAAA	TACTTTAAAT	GCTGCATT	TTATACAATC		2900	
ATTAATAGAA	TATAATAGTT	CTAAAGAAC	TCTTAGTAAT	TTAAGTGTAG		2950	
CAATGAAAGT	CCAAGTTAC	GCTCAATT	TTAGTACTGG	TTAAATACT		3000	
ATTACAGATG	CAGCCAAAGT	TGTTGAATTA	GTATCAACTG	CATTAGATGA		3050	
AACTATAGAC	TTACTTCTA	CATTATCTGA	AGGATTACCT	ATAATTGCAA		3100	
CTATTATAGA	TGGGTGTAAGT	TTAGGTGCAG	CAATCAAAGA	GCTAAGTGA		3150	
ACGAGTGACC	CATTATTAAG	ACAAGAAATA	GAAGCTAAGA	TAGGTATAAT		3200	
GGCAGTAAAT	TTAACAAACAG	CTACAACTGC	AATCATTACT	TCATCTTG		3250	
GGATAGCTAG	TGGATTAGT	ATACTTTAG	TTCTTTAGC	AGGAATTCA		3300	
GCAGGTATAC	CAAGCTTAGT	AAACAATGAA	CTTGTACTTC	GAGATAAGGC		3350	
AACAAAGGTT	GTAGATTATT	TTAAACATGT	TTCTTGTAGTT	GAAACTGAAG		3400	
GAGTATTAC	TTTATTAGAT	GATAAAATAA	TGATGCCACA	AGATGATT		3450	

GTGATATCAG	AAATAGATT	TAATAATAAT	TCAATAGTT	TAGGTAATG	3500
TGAAATCTGG	AGAATGGAAG	GTGGTTCAGG	TCATACTGTA	ACTGATGATA	3550
TAGATCACTT	CTTTTCAGCA	CCATCAATAA	CATATAGAGA	GCCACACTTA	3600
TCTATATATG	ACGTATTGGA	AGTACAAAAA	GAAGAACTTG	ATTGTCAAA	3650
AGATTTAATG	GTATTACCTA	ATGCTCCAAA	TAGAGTATT	GCTTGGGAAA	3700
CAGGATGGAC	ACCAGGTTA	AGAAGCTTAG	AAAATGATGG	CACAAAAGT	3750
TTAGACCGTA	TAAGAGATAA	CTATGAAGGT	GAGTTTATT	GGAGATATT	3800
TGCTTTATA	GCTGATGCTT	TAATAACAAC	ATTAAAACCA	AGATATGAAG	3850
ATACTAATAT	AAGAATAAAAT	TTAGATAGTA	ATACTAGAAAG	TTTATAGTT	3900
CCAATAATAA	CTACAGAATA	TATAAGAGAA	AAAATTATCAT	ATTCTTTCTA	3950
TGGTCAGGA	GGAACCTTATG	CATTGTCTCT	TTCTCAATAT	AATATGGGTA	4000
TAAATATAGA	ATTAAGTGAA	AGTGTGTTT	GGATTATAGA	TGTTGATAAT	4050
GTTGTGAGAG	ATGTAACAT	AGAATCTGAT	AAAATTAAAAA	AAGGTGATT	4100
AATAGAAGGT	ATTTTATCTA	CACTAAGTAT	TGAAGAGAAAT	AAAATTATCT	4150
TAAATAGCCA	TGAGATTAAT	TTTCTGGTG	AGGTAATGG	AAGTAATGGA	4200
TTTGTTCCTT	TAACATTTC	AATTTAGAA	GGAATAAATG	CAATTATAGA	4250
AGTTGATTTA	TTATCTAAAT	CATATAAATT	ACTTATTCT	GGCGAATTAA	4300
AAATATTGAT	GTAAATTC	AATCATATTC	AACAGAAAAT	AGATTATATA	4350
GGATTCAATA	GCGAATTACA	GAAAAATATA	CCATATAGCT	TTGTAGATAG	4400
TGAAGGAAAA	GAGAATGGTT	TTATTAATGG	TTCAACAAAAA	GAAGGTTTAT	4450
TTGTATCTGA	ATTACCTGAT	GTAGTTCTTA	TAAGTAAGGT	TTATATGGAT	4500
GATAGTAAGC	CTTCATTG	ATATTATAGT	AATAATTG	AAGATGTCAA	4550
AGTTATAACT	AAAGATAATG	TTAATATATT	AACAGGTTAT	TATCTTAAGG	4600
ATGATATAAA	AATCTCTT	TCTTGACTC	TACAAGATGA	AAAAACTATA	4650
AAGTTAAATA	GTGTGCATT	AGATGAAAGT	GGAGTAGCTG	AGATTTGAA	4700
GTTCATGAAAT	AGAAAAGGTA	ATACAAATAC	TTCAGATTCT	TTAATGAGCT	4750
TTTTAGAAAG	TATGAATATA	AAAAGTATT	TCGTTAATTT	CTTACAATCT	4800
AATATTAAGT	TTATATTAGA	TGCTAATTT	ATAATAAGTG	GTACTACTTC	4850
TATTGGCCAA	TTTGAGTTA	TTTGTGATGA	AAATGATAAT	ATACAACCAT	4900
ATTCATTAA	GTAAATACA	CTAGAAACTA	ATTATACTTT	ATATGTAGGA	4950
AATAGACAAA	ATATGATAGT	GGAACCAAAT	TATGATTTAG	ATGATTCTGG	5000
AGATATATCT	TCAACTGTTA	TCAATTCTC	TCAAAAGTAT	CTTTATGGAA	5050
TAGACAGTTG	TGTTAATAAA	GTTGTAATT	CACCAAATAT	TTATACAGAT	5100
GAAATAAATA	TAACGCCGT	ATATGAAACA	AATAACTT	ATCCAGAAGT	5150
TATTGTATTA	GATGCAAATT	ATATAATGA	AAAATAAAAT	GTAAATATCA	5200
ATGATCTATC	TATACGATAT	GTATGGAGTA	ATGATGGTAA	TGATTTTATT	5250
CTTATGTCAA	CTAGTGAAGA	AAATAAGGTG	TCACAAGTTA	AAATAAGATT	5300
CGTTAATGTT	TTTAAAGATA	AGACTTTGGC	AAATAAGCTA	TCTTTAACT	5350
TTAGTGATAA	ACAAGATGTA	CCTGTAAGTG	AAATAATCTT	ATCATTACAA	5400
CCTTCATATT	ATGAGGATGG	ATTGATTGGC	TATGATTGG	GTCTAGTTTC	5450
TTTATATAAT	GAGAAATT	ATATTAATAA	CTTGGAAATG	ATGGTATCTG	5500
GATTAATATA	TATTAATGAT	TCATTATATT	ATTTAAACC	ACCAGTAAAT	5550
AATTTGATAA	CTGGATTG	GACTGTAGGC	GATGATAAAT	ACTACTTTAA	5600
TCCAATTAAAT	GGTGGAGCTG	CTTCAATTGG	AGAGACAATA	ATTGATGACA	5650
AAAATTATTA	TTTCAACCAA	AGTGGAGTGT	TACAAACAGG	TGTATTTAGT	5700
ACAGAAGATG	GATTAAATA	TTTGCCCCA	GCTAATACAC	TTGATGAAA	5750
CCTAGAAGGA	GAAGCAATTG	ATTTTACTGG	AAAATTAAATT	ATTGACGAAA	5800
ATATTATTA	TTTGATGAT	AATTATAGAG	GAGCTGTAGA	ATGGAAAGAA	5850
TTAGATGGTG	AAATGCACTA	TTTGGCCCCA	GAAACAGGTA	AAGCTTTAA	5900
AGGTCTAAAT	CAAATAGGTG	ATTATAAATA	CTATTTCAAT	TCTGATGGAG	5950
TTATGCAAAA	AGGATTGTT	AGTATAAATG	ATAATAACAA	CTATTTTGAT	6000
GATTCTGGTG	TTATGAAAGT	AGGTTACACT	GAAATAGATG	GCAAGCATTT	6050
CTACTTTGCT	GAAAACGGAG	AAATGCAAAT	AGGAGTATT	AATACAGAAG	6100
ATGGATTAA	ATATTTGCT	CATCATAATG	AAGATTTAGG	AAATGAAGAA	6150
GGTGAAGAAA	TCTCATATT	TGGTATATT	AATTCATAA	ATAAAATTAA	6200
CTATTTGAT	GATTCAATT	CAGCTGTAGT	TGGATGGAAA	GATTTAGAGG	6250
ATGGTTCAAA	GTATTATTT	GATGAAGATA	CAGCAGAAGC	ATATATAGGT	6300

TTGTCATTAA	TAAATGATGG	TCAATATTAT	TTTAATGATG	ATGGAATTAT	6350
GCAAGTTGGA	TTTGTCACTA	TAAATGATAA	AGTCTTCTAC	TTCTCTGACT	6400
CTGGAATTAT	AGAATCTGGA	GTACAAAACA	TAGATGACAA	TTATTTCTAT	6450
ATAGATGATA	ATGGTATAGT	TCAAATTGGT	GTATTTGATA	CTTCAGATGG	6500
ATATAAATAT	TTTGCACCTG	CTAATACTGT	AAATGATAAT	ATTTACGGAC	6550
AAGCAGTTGA	ATATAGTGGT	TTAGTTAGAG	TTGGGGAAAGA	TGTATATTAT	6600
TTTGGAGAAA	CATATACAAT	TGAGACTGGA	TGGATATATG	ATATGGAAAA	6650
TGAAAGTGAT	AAATATTATT	TCAATCCAGA	AACTAAAAAA	GCATGCAAAG	6700
GTATTAATT	AATTGATGAT	ATAAAATATT	ATTTTGATGA	GAAGGGCATA	6750
ATGAGAACGG	GTCTTATATC	ATTTGAAAAT	AATAATTATT	ACTTTAATGA	6800
GAATGGTGAA	ATGCAATTG	GTTATATAAA	TATAGAAGAT	AAGATGTTCT	6850
ATTTTGGTGA	AGATGGTGT	ATGCAGATTG	GAGTATTTAA	TACACCAGAT	6900
GGATTTAAAT	ACTTTGCACA	TCAAAATACT	TTGGATGAGA	ATTTGAGGG	6950
AGAATCAATA	AACTATACTG	GTTGGTTAGA	TTTAGATGAA	AAGAGATATT	7000
ATTTTACAGA	TGAATATATT	GCAGCAACTG	GTTCAGTTAT	TATTGATGGT	7050
GAGGAGTATT	ATTTTGATCC	TGATACAGCT	CAATTAGTGA	TTAGTGAATA	7100
G					7101

## 2) INFORMATION FOR SEQ ID NO: 2131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131

AAGCMATTGT TGTAAATTAA GAAAG

25

## 2) INFORMATION FOR SEQ ID NO: 2132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132

TCATATCCAT AGCAATAGTT CTA

23

## 2) INFORMATION FOR SEQ ID NO: 2133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid

1100

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133

CCACGCACAW AAACTTGTTT TAGAAGTAGC AGCWCAGCGT GG

42

2) INFORMATION FOR SEQ ID NO: 2134

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134

CGCGTGAAGC TTCTGTG

17

2) INFORMATION FOR SEQ ID NO: 2135

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135

TCTCGCCGTT ATTCAAGTTTC

20

2) INFORMATION FOR SEQ ID NO: 2136

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136

CCAACGCGTC CTCAATCATT TCTAACTTCT ATGGCCGGCG TTGG

44

## 2) INFORMATION FOR SEQ ID NO: 2137

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 889 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas putida*
  - (C) ACCESSION NUMBER: Genome project
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137

ATGATCACCG	GTGCTGCCCA	GATGGACGGC	GCGATCCTGG	TTTGCTCGGC	50
CGCCGATGGT	CCGATGCCrC	AAACCCGTGA	GCACATCCTG	CTGTCCCGTC	100
AGGTAGGCGT	TCCGTACATC	GTGGTCTTCC	TGAACAAAGGC	CGACCTGGTA	150
GACGACGCTG	AGCTGCTGGA	ACTGGTCGAG	ATGGAAGTTC	GCGACCTGCT	200
GTCCACCTAC	GACTTCCCAG	GCGACGACAC	TCCGATCATC	ATCGGTTCCG	250
CTCGTATGGC	CCTGGAAAGGC	AAAGACGACA	ACGAAATGGG	CACTACCGCT	300
GTCAAGAACG	TGGTAGAAAC	TCTGGATGCC	TACATCCCTG	AGCCAGTTCG	350
TGCCATCGAC	CAGCCGTTCC	TGATGCCGAT	CGAAGACGTG	TTCTCGATCT	400
CGGGTCTG	TACCGTTGTT	ACCGGTCGTA	TCGAGCGTGG	CATCGTTCGC	450
GTTCAGGATC	CGCTGGAAAT	CGTTGGTCTG	CGTGACACCA	CCACCAACAC	500
CTGCACCGGT	GTTGAGATGT	TCCGCAAGCT	GCTGGACGAA	GGTCGTGCTG	550
GCGAGAACTG	CGGGCGTTCTG	CTGCGTGGTA	CCAAGCGTGA	CGACGTTGAG	600
CGTGGCCAGG	TTCTGGTCAA	GCCAGGTTCG	GTCAAGCCGC	ACACCAAGTT	650
CACCGCAGAA	GTCTACGTCC	TGTCGAAGGA	AGAAGGCGGC	CGTCACACTC	700
CGTTCTTCAA	AGGCTACCGT	CCACAGTTCT	ACTTCCGTAC	CACTGACGTG	750
ACCGGTAAC	GCGAACTGCC	GGAAAGGCCTT	GAAATGGTAA	TGCCAGGTGA	800
CAACATTCAG	ATGACTGTTA	CCCTGATCAA	GACCATCGCA	ATGGAAGACG	850
GTCTGCGCTT	CGCTATCCGT	GAAGGGCGTC	GTACCGTCG		889

## 2) INFORMATION FOR SEQ ID NO: 2138

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 900 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Pseudomonas aeruginosa*
  - (B) STRAIN: PAO-1
  - (C) ACCESSION NUMBER: Genome project
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138

AACATGATCA	CCGGTGCTGC	CCAGATGGAC	GGCGCGATCC	TGGTTGCTC	50
GGCTGCCGAC	GGCCCCATGC	CGCAGACCCG	CGAGCACATC	CTGCTGTCCC	100
GCCAGGTAGG	CGTTCCTAC	ATCGTCGTGT	TCCTGAACAA	GGCCGACATG	150
GTCGACGACG	CCGAGCTGCT	GGAACGGTC	GAGATGGAAG	TTCCGCGATCT	200
GCTGAACACC	TACGACTTCC	CGGGCGACGA	CACTCCGATC	ATCATCGGTT	250
CCGCGCTGAT	GGCGCTGGAA	GGCAAGGATG	ACAACGGCAT	CGGCCTAAGC	300
GCCGTGCAGA	AGCTGGTACA	GACCCTGGAC	TCCTACATT	CGGAGCCGGT	350
TCGTGCCATC	GACCAGCCGT	TCCTGATGCC	GATCGAAGAC	GTGTTCTCGA	400
TCTCCGGCCG	CGGTACCGTG	GTAACCGGTC	GTGTAGAGCG	CGGCATCATC	450
AAGGTCCAGG	AAGAAGTGGA	AATCGTCGGC	ATCAAGGCGA	CCACCAAGAC	500
TACCTGCACC	GGCGTTGAAA	TGTTCCGCAA	GCTGCTCGAC	GAAGGTCGTG	550
CTGGTGAGAA	CGTTGGTATC	CTGCTGCGTG	GCACCAAGCG	TGAAGACGTA	600
GAGCGTGGCC	AGGTTCTGGC	CAAGCCGGGC	ACCATCAAGC	CGCACACCAA	650
GTTCGAGTGC	GAAGTGTACG	TGCTGTCCAA	GGAAAGAAGGT	GGTCGTCACA	700
CCCCGTTCTT	CAAGGGCTAC	CGTCCGCACT	TCTACTTCCG	TACCACCGAC	750
GTGACCGGTA	ACTGCGAACT	GCCGGAAGGC	GTAGAGATGG	TAATGCCGGG	800
CGACAACATC	AAAGATGGTTG	TCACCCCTGAT	CGCTCCGATC	GCCATGGAAG	850
ATGGCCTGCG	CTTCGCGATC	CGCGAAGGCG	GCCGTACCGT	TGGCGCCGGC	900

## 2) INFORMATION FOR SEQ ID NO: 2139

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni*
- (B) STRAIN: NCTC 11168
- (C) ACCESSION NUMBER: AL139074

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139

ATGCAAGGAT	TTATTTCACA	GGTATTAGGT	CCGGTTGTTG	ATGTAGATT	50
TAACGACTAT	TTGCCTCAAA	TTAATGAAGC	AATTGTTGTA	AATTTTGAAA	100
GCAGAAGAAA	AAAACATAAA	CTTGTGTTAG	AAGTAGCAGC	TCATTTAGGA	150
GATAATAGAG	TTAGAACTAT	TGCTATGGAT	ATGACAGATG	GTTTGGTAAG	200
GGGCTTAAAA	GCTGAGGCTT	TAGGTGCTCC	CATTAGTGT	CCTGTTGGTG	250
AGAAAGTTTT	AGGAAGAATT	TTCAATGTTA	CTGGAGATTT	GATCGATGAA	300
GGTGAAGAAA	TTTCTTCGA	TAACAAATGG	GCAATTCTATA	GAGATCCACC	350
AGCTTTGAA	GATCAAAGCA	CAAAAGTGA	GATTTTGAA	ACAGGGATTA	400
AAGTTGTAGA	TTTACTTGCT	CCTTATGCAA	AAGGTGGTAA	AGTAGGTCTT	450
TTTGGTGGTG	CAGGTGTTGG	TAACAACTGTT	ATTATTATGG	AGCTTATTCA	500
CAATGTTGCA	TTAACGATA	GGGGCTATTC	TGTATTTGCA	GGTGTGGGTG	550
AGAGAACTCG	TGAAGGAAAT	GACCTTTATA	ATGAAATGAA	AGAAAGTAAT	600
GTTTAGACA	AAGTTGCTCT	ATGTTATGGA	CAAATGAATG	AACCACCAAG	650
GGCAAGAAAT	CGTATTGCTT	TAACAGGTTT	AACAATGGCT	GAGTATTTA	700
GAGATGAAAT	GGGTCTTGAT	GTGCTTATGT	TTATTGATAA	TATCTTACA	750
TTTCACAAT	CAGGTTCTGA	AATGTCAGCA	CTTTAGGAA	GAATTCCATC	800
AGCTGTGGGT	TATCAACCAA	CCTTAGCAAG	TGAAATGGGT	AAATTCCAAG	850
AAAGAATTAC	TTCAACTAAA	AAAGGCTCAA	TCACCTCAGT	TCAAGCTGTT	900
TACGTTCCAG	CTGATGACTT	AACAGACCCA	GCTCCAGCAA	CTGTTTTGTC	950

TCACCTTAGAT	GCTACAAACGG	TTTTAAATAG	AGCTATTGCT	GAAAAGGGTA	1000
TTTATCCTGC	AGTTGACCCA	CTTGACTCAA	CTTCAAGAAT	GCTTGACCCA	1050
AATATCATTG	GAGAAGAACCA	TTATAAAGTT	GCTCGTGGTG	TTCAATCAGT	1100
GCTTCAAAAA	TACAAAGATT	TACAAGATAT	CATGCCATT	TTAGGTATGG	1150
ATGAGCTTAG	CGAAGAGGAT	AAACTTGTAG	TTGAAAGAGC	AAGAAAGATT	1200
AAAAAAATTCT	TATCACAAACC	ATTTCGTT	GCAGAAGTTT	TCACAGGTAG	1250
CCCAGGAAAA	TATATAAGCC	TTGAAGATAC	AATAGCAGGA	TTTAAGGGAA	1300
TTTTAGAAGG	AAATATGAT	CATTTACCAAG	AAAATGCTTT	CTATATGGTT	1350
GGAAATATAG	ATGAAGCTAT	TGCAAAAGCG	GATAAATTAA	AAGGTTAA	1398

## 2) INFORMATION FOR SEQ ID NO: 2140

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2157 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*
- (B) STRAIN: 670
- (C) ACCESSION NUMBER: X67867

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140

ATGAACAAAC	CAACGATTCT	GCGCCTAATC	AAGTATCTGA	GCATTAGCTT	50
CTTAAGCTTG	GTTATCGCAG	CCATTGTCTT	AGGCGGAGGA	GTTCAGTTCT	100
ACTACGTTAG	CAAGGCTCCT	AGCCTATCCG	AGAGTAAACT	AGTTGCAACA	150
ACTTCTAGTA	AAATCTACGA	CAATAAAAAT	CAACTCATG	CTGACTTGGG	200
TTCTGAACGC	CGCGTCAATG	CCCAAGCTAA	TGATATTCCC	ACAGATTGG	250
TTAAGGCAAT	CGTTTCTATC	GAAGACCATC	GCTTCTTCGA	CCACAGGGGG	300
ATTGATTCCA	TCCGTATCCT	GGGAGCTTC	TTGCGCAATC	TGCAAAGTAA	350
TTCCCTCCAA	GGTGGATCAA	CTCTCACCCA	ACAGTTGATT	AAGTTGACTT	400
ACTTTTCAAC	CTCGACTTCC	GACCAGACTA	TTTCTCGTA	GGCTCAGGAA	450
GCTTGGTTAG	CGATTCAAGT	AGAACAAAAA	GCAACCAAAC	AGGAAATCTT	500
GACCTACTAT	ATAAAATAAGG	TCTACATGTC	TAATGGCAAC	TATGGAATGC	550
AGACAGCAGC	TCAAAACTAC	TATGGTAAAG	ACCTCAATAA	TTTAAGTTA	600
CCTCAGTTAG	CCTTGCTGGC	TGGAATGCCT	CAGGCACCAA	ACCAATATGA	650
CCCCTATTCA	CATCCAGAAG	CAGCCCAGA	CCGCCGAAAC	TTGGTCTTAT	700
CTGAAATGAA	AAATCAAGGT	TACATCTCTG	CTGAACAGTA	TGAGAAAGCA	750
GTCAATACAC	CAATTACTGA	TGGACTACAA	AGTCTCAAAT	CAGCAAGTAA	800
TTACCCGT	TACATGGATA	ATTACCTCAA	GGAGGTCAATC	AATCAAAGTAG	850
AACAAGAAAC	TGGCTATAAC	CTTCTAACTA	CTGGGATGGA	TGTTTACACA	900
AATGTAGACC	AAGAAGCTCA	AAAACATCTG	TGGGATATCT	ACAACCTCCGA	950
TCAATACGTC	TCTTACCCCTG	ACGATGATTT	GCAAGTCGCA	TCTACGGTCG	1000
TAGATGTTTC	AAATGGTAAA	GTCATCGCCC	AACTTGGAGC	TCGTCACCAA	1050
GCAAGTAACG	TTTCATTTGG	TACCAACCAA	GCTGTGGAAA	CCAATCGTGA	1100
CTGGGGTTCT	GCTATGAAAC	CAATCACCAG	TTATGCACCT	GCCATAGAAAT	1150
ACGGTGTGAA	TGATTCCACT	GCAACTATGG	TAAATGATAT	TCCTTATAAC	1200
TATCCGGAA	CAAGCACACC	TGTCTACAAC	TGGGATAGAG	CATATTCGG	1250
TAATATTACT	CTGCAATATG	CTCTTCAACA	ATCACGAAAT	GTCACAGCCG	1300
TTGAGACTTT	GAATAAGGTC	GGTCTAGATA	GAGCTAAAAC	CTTCCTTAAT	1350
GGTCTTGGTA	TCGACTATCC	AAGCATGCAT	TATGCAAACG	CCATTCAAG	1400

TAATACAACA	GAATCTAATA	AACAATACGG	AGCAAGTAGT	GAAAAAAATGG	1450
CTGCTGCCTT	TGCTGCCTT	GCCAACGGTG	GAATTTACCA	CAAACCCATG	1500
TATATCAATA	AGGTCGTCTT	CAGTGACGGT	AGTAAAAAAAG	AATTTCAGA	1550
TGTAGGTACA	CGAGCTATGA	AAGAAACAAAC	TGCTTACATG	ATGACCGAAA	1600
TGATGAAAAC	TGTCTGGCA	TACGGAACGT	GTCGTGGAGC	CTATCTCCC	1650
TGGTTAGCGC	AAGCTGGTAA	GACAGGGTACT	TCTAACTACA	CAGATGATGA	1700
AATTGAAAAA	CACATCAAGA	ACACTGGCTA	TGTAGCTCCA	GATGAAATGT	1750
TTGTTGGTTA	TACTCGTAAG	TATTCTATGG	CTGTATGGAC	AGGTTATTG	1800
AATCGTTAA	CTCCTATCGT	TGGAGATGGT	TTCCTAGTTG	CAGCTAAAGT	1850
TTATCGCTCA	ATGATAACGT	ATCTATCAGA	AGATACTCAT	CCAGAAGACT	1900
GGACGATGCC	AGACGGACTT	TTCAAGAACG	GGGAATTGTT	ATTCAAAAAT	1950
GGAGCTCGTT	CTACGTGGAG	CTCACCTGCT	CCACAAACAAAC	CCCCATCAAC	2000
TGAAAGTTCA	AGCTCATCAT	CAGATAGTTC	AACTTCACAG	TCTAGCTCAA	2050
CCACTCCAAG	CACAAATAAT	AGTACGACTA	CCGATCCTAA	CAATAATACG	2100
CAACAATCAA	ATACAACCCC	TGATCAACAA	AATCAGAATC	CTCAACCAGC	2150
					2157
	ACAAACCA				

## 2) INFORMATION FOR SEQ ID NO: 2141

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141

CACCAAGTCAC AGAAAAGC

18

## 2) INFORMATION FOR SEQ ID NO: 2142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142

GCCTTAATTG CGGATAGTGC

20

## 2) INFORMATION FOR SEQ ID NO: 2143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1105

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143

GAGAAAGAGC CCAATTATCT AATGT

25

2) INFORMATION FOR SEQ ID NO: 2144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3075 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: J2870
- (C) ACCESSION NUMBER: X75439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144

TTGACAAAGA	AATATTTAAA	CACCCAGAAT	GAAATATCAG	CATTTGGAA	50
TACTCAAAG	ATATTTAAA	AATCAATTGA	CAATAGAAAA	GGACAGGAAA	100
GTGTTGTTT	TTATGACGGC	CCCCCAACTG	CAAATGCCCT	TCCTCATGCT	150
GGCCATGTTC	TTGGAAGAGT	AATCAAGGAT	TTAGTTGCAA	GATTAAAAAC	200
TATGCAAGGT	TTTTATGTAG	AAAGAAAAGC	AGGATGGGAT	ACCCATGGCT	250
TACCAAGTTGA	ATTAGAGGTT	AAAAAAGAAA	TTGGAATTAA	AGGAAAACAA	300
GACATTGAAA	AGTATGGAAT	AGAAAATTTT	ATAAAATGAAT	GTAAAAAAAG	350
TGTATTAAAT	TATGAAAAAG	AATGGCGGGA	TTTTTCTAAA	GATTTAGGAT	400
ACTGGGTTGA	CATGGACTCC	CCCTATATAA	CTCTTGAGAA	TAATTATATT	450
GAAAGTGTAT	GGAATATATT	ATCTACATTC	CATAAAAAG	GACTATTATA	500
TAAGGGACAT	AAGGTGACTC	CTTATTGTAC	ACATGATCAA	ACCGCTTTAA	550
GTTCTCATGA	AGTAGCGCAA	GGCTATAAAA	ACGTTAAAGA	TTTATCAGCT	600
GTTGTTAAAT	TTCAACTTAC	AAATAGTAAA	GATACTTATT	TCTTAAGTTG	650
GACTACCACT	CCCTGGACTT	TGCCTGCAA	TGTAGCATTA	GCTATAAATA	700
AAGATCTTAA	TTATTCAAAA	ATTCGGGTAG	AAAATGAGTA	TTATATCTTA	750
GCTACAGATC	TAATTAATTC	TATAATAACT	GAAAATACG	AAATTATTGA	800
TACCTTTCA	GGAAGTAATT	TAATTAATT	AAAATACATT	CCTCCTTTG	850
AAAGCGACGG	TTTAGTTAAT	GCATATTACG	TTGTTGATGG	AGAATTGTT	900
ACTAACTCAG	AAGGAACTGG	TATTGTTCAT	ATAGCACCAAG	CTCATGGGA	950
AGATGACTAC	CAATTGGTTT	TAGAGCGTGA	TTTGGATTTC	TTAAATGTTA	1000
TAACAAGAGA	AGGAGTATAT	AATGATAGGT	TCCCTGAATT	AGTTGGTAAT	1050
AAAGCTAAAA	ATAGTGATAT	AGAAATCATA	AAATTATTAT	CCAAAAAAACA	1100
ACTTTTATAT	AAAAAACAAA	AATATGAGCA	TAATTATCCT	CATTGTTGGA	1150
GATGTGGTAA	TCCTTGATA	TATTATGCGA	TGGAAGGTTG	GTGTTATTAAA	1200
ACAACTAATT	TTAAGAATGA	AATTATTAAC	ATAATAATA	ATATAGAGTG	1250
GTTTCCCTCT	CATATTAAGG	AAGGGAGAAT	GGGAAATTTC	TTAGAAAATA	1300
TGGTTGATTG	GAACATTGGT	AGAAATAGAT	ATTGGGGAAC	ACCATTAAAT	1350
GTATGGATT	GCAATGATTG	TAATCACGAA	TACGCACCAA	GTAGTATTAA	1400
GGATTACAA	AATAATTCCA	TCAATAAAAT	TGATGAAGAT	ATTGAGTTGC	1450
ATAGACCTTA	TGTTGATAAT	ATCACTCTTA	GTGCCCCCTAA	GTGTAATGGG	1500

1106

AAAATGTCTC	GAGTAGAAGA	AGTAATCGAT	GTTTGGTTG	ATAGCGGCTC	1550
TATGCCGTTT	GCTCAGCATC	ATTATCCTTT	TGATAACCAG	AAAATTTTA	1600
ATCAACACTT	TCCAGCTGAT	TTTATTGCAG	AAGGAGTTGA	TCAAACGAGA	1650
GGCTGGTTT	ACAGTTTACT	AGTAATTCT	ACTATTCTAA	AAGGAAAATC	1700
TTCTTATAAA	CGTGCTTAT	CTTTAGGACA	TATTCTAGAC	AGTAATGGTA	1750
AAAAAATGTC	TAAGAAGTAAA	GGAAACGTTA	TTAATCCAAC	TGAATTAATT	1800
AATAAGTACG	GAGCCGATTC	TTTAAGATGG	GCCTTAATT	CGGATAGTGC	1850
TCCATGGAAT	AAACAAAAGAT	TCTCAGAAAA	TATAGTAGCT	CAGACCAAAT	1900
CGAAATTAT	AGATACGCTT	GATAATATT	ATAAATTAA	TAATATGTAT	1950
AATAAAATAG	ATCACTATAA	TCCTAATAAT	GAAATTACAA	AAAGTAGAAA	2000
TACATTAGAT	AATTGGGCTC	TTTCTCGCTT	AAACACCTTA	ATAAAAGAAA	2050
GTAATATTAA	TGTAAATAAT	TACGATTCA	CTTCCGCAGC	CAGATTAATT	2100
AACGAATATA	CCAATACAAT	AAGTAATTGG	TATATCGGAG	ATTGAGAGG	2150
ACGATTTGG	GAACAAAGGAA	TTTCTAACGA	AAAAAAAGAT	GCGTACAATA	2200
CGCTTTATGA	AATTTTAACA	ACTTTATCAA	GAACATGGC	TCCATTGTT	2250
CCATTTATAT	CTGAAAAAAAT	CCATTATAAT	TTGACTGGAA	AAAGTGTGCA	2300
TTTACAAGAT	TATCCACAAAT	ATAAAGAAAG	TTTATTAAAT	CAAGCATTGG	2350
AAGATGAAAT	GCATACCGTT	ATAAAAATTG	TAGAATTATC	TAGACAGGCT	2400
CGCAAAAATG	CAGATTAAA	AATTAAGCAA	CCTTTATCGA	AAATGGTGT	2450
TAAACCTAAT	AGTCAATTAA	ACTTAAGTTT	TTTACCTAAT	TACTATTCAA	2500
TAATAAAAGA	CGAATTAAAT	ATAAAAAAACA	TTGAATTAAC	TGATAATATT	2550
AATGACTATA	TTACCTATGA	GCTTAAATTG	AATTTTTCTT	CTGTGGGACC	2600
AAAACCTAGGG	AACAAAACGA	AAAATATTCA	AACATTGATA	GAACCCCTAT	2650
CAGAGTATGA	TAACAAAGT	TTAATTGAGT	CTAATAACTT	CAAAAGTTA	2700
TCTTCTGATG	CTGAGTTAAC	TAAGGATGAT	TTTATAATT	AAACCTTACC	2750
TAAGGATAGT	TATCAACTCA	GTGAAGATAA	TGACTGCCTT	ATATTATTAG	2800
ATAAAAATT	ATCTCCTGAA	TTAATTGCG	AAGGACATGC	TAGAGAGCTC	2850
ATTAGATTAA	TTCAACAAATT	AAGAAAAAAAG	AAAATTTAC	CAATAAAATCA	2900
ACGTATTGAT	ATTTATATCG	GTGTAACTGG	GGAATTATTA	GAATCAATAA	2950
AAACCAATAA	AAATATGTTT	AAAGAAAATT	TCGTGATTAA	AAATATACAC	3000
TTAAATGTTA	TAGATGAATA	TGAAAATACT	ATTCAATTAA	ATAATAAAGA	3050
AATAAAAATT	TCCTTATTAT	ATTAA			3075

## 2) INFORMATION FOR SEQ ID NO: 2145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145

GCAAGATGTG GCGTGTACG GT

22

## 2) INFORMATION FOR SEQ ID NO: 2146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

1107

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146

GGGGCGAAGA AGTTGTCCAT ATT

23

2) INFORMATION FOR SEQ ID NO: 2147

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Escherichia coli*

(C) ACCESSION NUMBER: V00622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147

ATGGAGAAAA AAATCACTGG ATATACCACC GTTGATATAT CCCAATGGCA	50
TCGTAAAGAA CATTTCAGGG CATTTCAGTC AGTTGCTCAA TGTACCTATA	100
ACCAGACCGT TCAGCTGGAT ATTACGGCCT TTTTAAAGAC CGTAAAGAAA	150
AATAAGCACA AGTTTTATCC GGCCTTTATT CACATTCTG CCCGCCTGAT	200
GAATGCTCAT CCGGAATTCC GTATGGCAAT GAAAGACGGT GAGCTGGTGA	250
TATGGGATAG TGTTCACCCCT TGTTACACCG TTTTCCATGA GCAAACGTGAA	300
ACGTTTCAT CGCTCTGGAG TGAATACACAC GACGATTTCC GGCAGTTTCT	350
ACACATATAT TCGCAAGATG TGGCGTGTAA CGGTGAAAAC CTGGCCTATT	400
TCCCTAAAGG GTTTATTGAG AATATGTTT TCCTCTCAGC CAATCCCTGG	450
GTGAGTTTCA CCAGTTTGA TTTAAACGTG GCCAATATGG ACAACTTCTT	500
CGCCCCCGTT TTCACCATGG GCAAATATTA TACGCAAGGC GACAAGGTGC	550
TGATGCCGCT GGCGATTTCAG GTTCATCATG CCGTCTGTGA TGGCTTCCAT	600
GTCGGCAGAA TGCTTAATGA ATTACAACAG TACTGCGATG AGTGGCAGGG	650
CGGGCGTAA	660

2) INFORMATION FOR SEQ ID NO: 2148

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148

CAGATTAAT GCGGATTTCAG CC

22

## 2) INFORMATION FOR SEQ ID NO: 2149

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149

ATCAGGTAAA TCATCAGCGG ATA

23

## 2) INFORMATION FOR SEQ ID NO: 2150

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 642 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Escherichia coli*
  - (B) STRAIN: K12
  - (C) ACCESSION NUMBER: X53796
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150

ATGAATTTA	CCCGGATTGA	CCTGAATACC	TGGAATCGCA	GGGAACACTT	50
TGCCCTTAT	CGTCAGCAGA	TTAAATGCGG	ATTCAAGCTG	ACCACCAAAAC	100
TCGATATTAC	CGCTTGCCTG	ACCGCACTGG	CGGAGACAGG	TTATAAGTTT	150
TATCCGCTGA	TGATTTCACCT	GATCTCCGG	GCTGTTAAC	AGTTTCCGGA	200
GTTCCGGATG	GCACGTAAAG	ACAATGAAC	TATTTACTGG	GACCAGTCAG	250
ACCCGGTCTT	TACTGTCTTT	CATAAAGAAA	CCGAAACATT	CTCTGCACTG	300
TCCTGCCGTT	ATTTTCCGGA	TCTCAGTGAG	TTTATGGCAG	GTTATAATGC	350
GGTAACGGCA	GAATATCAGC	ATGATACCAAG	ATTGTTTCCG	CAGGGAAATT	400
TACCGGAGAA	TCACCTGAAT	ATATCATCAT	TACCGTGGGT	GAGTTTTGAC	450
GGATTTAAC	TGAACATCAC	CGGAAATGAT	GATTATTTG	CCCCGGTTT	500
TACGATGGCA	AAGTTTCAGC	AGGAAGGTGA	CCCGGTATTA	TTACCTGTTT	550
CTGTACAGGT	TCATCATGCA	GTATGTGATG	GCTTCATGC	AGCACGGTTT	600
ATTAATACAC	TTCAGCTGAT	GTGTGATAAC	ATACTGAAAT	AA	642

## 2) INFORMATION FOR SEQ ID NO: 2151

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 bases
  - (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151

ATATTCAGC ATTACCTTGG GTT

23

2) INFORMATION FOR SEQ ID NO: 2152

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152

TACACAACTC TTGTAGCCGA TTA

23

2) INFORMATION FOR SEQ ID NO: 2153

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 642 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Shigella flexineri*
  - (C) ACCESSION NUMBER: X07848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153

ATGAACATA CAAAATTGATGTAAAAAT	TGGGTTCGCC GTGAGCATT	50
TGAGTTTAT CGGCATCGTT TACCATGTGG TTTTAGCTTA ACAAGCAAA		100
TTGATATCAC GACGTTAAAA AAGTCATTGG ATGATTCAAGC GTATAAGTT		150
TATCCGTAA TGATCTATCT GATTGCTCAG GCCGTGAATC AATTGATGA		200
GTTGAGAATG GCGATAAAAG ATGATGAATT GATCGTATGG GATTCACTCG		250
ACCCACAATT CACCGTATTC CATCAAGAAA CAGAGACATT TTCAGCACTG		300
AGTTGCCAT ACTCATCCGA TATTGATCAA TTTATGGTGA ATTATTTATC		350
GGTAATGGAA CGTTATAAAA GTGATACCAA GTTATTCTTCAAGGGTAA		400
CACCAAGAAA TCATTTAAAT ATTTCAAGCAT TACCTGGGT TAATTTGAT		450
AGCTTAAATT TAAATGTTGC TAATTTTACCA GATTATTTG CACCCATTAT		500
AACAATGGCA AAATATCAGC AAGAAGGGGA TAGACTGTTA TTGCCGCTCT		550
CAGTACAGGT TCATCATGCA GTTGTGATG GCTTCCATGT TGACAGCTTT		600
ATTAATCGGC TACAAGAGTT GTGTAACAGT AAATTAAAAT AA		642

## 2) INFORMATION FOR SEQ ID NO: 2154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154

CGCCATTAG AGTTAGGAC

20

## 2) INFORMATION FOR SEQ ID NO: 2155

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155

TTCCATACCG TTGCGTATCA CTT

23

## 2) INFORMATION FOR SEQ ID NO: 2156

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium perfringens*
- (B) STRAIN: CP590
- (C) ACCESSION NUMBER: M74769

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156

ATGGTATTG AAAAATTGA TAAAAATAGT TGGAACAGAA AAGAGTATT	50
TGACCACTAC TTTGCAAGTG TACCTTGAC ATACAGCATG ACCGTTAAAG	100
TGGATATCAC ACAAAATAAG GAAAAGGGAA TGAAAATATA TCCTGCAATG	150
CTTTATTATA TTGCAATGAT TGTAAACCGC CATTCAGAGT TTAGGACGGC	200
AATCAATCAA GATGGTGAAT TGGGGATATA TGATGAGATG ATACCAAGCT	250

1111

ATACAATATT	TCACAATGAT	ACTGAAACAT	TTTCCAGCCT	TTGGACTGAG	300
TGTAAGTCTG	ACTTTAACATC	ATTTTAGCA	GATTATGAAA	GTGATACGCA	350
ACGGTATGGA	AAACATCATA	GAATGGAAGG	AAAGCCAAAT	GCTCCGGAAA	400
ACATTTTAA	TGTATCTATG	ATACCGTGGT	CAACCTTCGA	TGGCTTTAAT	450
CTGAATTGCA	AGAAAGGATA	TGATTATTG	ATTCCCTATT	TTACTATGGG	500
GAAATATTAT	AAAGAAGATA	ACAAAATTAT	ACTTCCTTTG	GCAATTCAAG	550
TTCATCACGC	AGTATGTGAC	GGATTCACA	TTTGCCTTT	TGTAAACGAA	600
TTGCAGGAAT	TGATAAATAG	TTAA			624

## 2) INFORMATION FOR SEQ ID NO: 2157

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157

CCACAGAAAT TGATATTAGT GTTTTAT

27

## 2) INFORMATION FOR SEQ ID NO: 2158

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158

TCGCTATTGT AACCAAGTTCT A

21

## 2) INFORMATION FOR SEQ ID NO: 2159

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: V01277

1112

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159

ATGAACTTTA	ATAAAATTGA	TTTAGACAAT	TGGAAGAGAA	AAGAGATATT	50
TAATCATTAT	TTGAACCAAC	AAACGACTTT	TAGTATAACC	ACAGAAATTG	100
ATATTAGTGT	TTTATACCGA	AACATAAAAC	AAGAAGGATA	TAAATTTAC	150
CCTGCATTTA	TTTCTTAGT	GACAAGGGTG	ATAAACTCAA	ATACAGCTT	200
TAGAACTGGT	TACAATAGCG	ACGGAGAGTT	AGGTTATTGG	GATAAGTTAG	250
AGCCACTTTA	TACAATTTT	GATGGTGTAT	CTAAAACATT	CTCTGGTATT	300
TGGACTCCTG	TAAAGAATGA	CTTCAAAGAG	TTTATGATT	TATACCTTC	350
TGATGTAGAG	AAATATAATG	GTTCGGGGAA	ATTGTTTCCC	AAAACACCTA	400
TACCTGAAAA	TGCTTTTCT	CTTCTATTA	TTCCATGGAC	TTCATTTACT	450
GGGTTTAACT	TAAATATCAA	TAATAATAGT	AATTACCTTC	TACCCATTAT	500
TACAGCAGGA	AAATTCACTA	ATAAAAGGTA	TTCAATATAT	TTACCGCTAT	550
CTTTACAGGT	ACATCATTCT	GTTTGTGATG	GTTATCATGC	AGGATTGTTT	600
ATGAACTCTA	TTCAGGAATT	GTCAGATAGG	CCTAATGACT	GGCTTTATA	650
A					651

## 2) INFORMATION FOR SEQ ID NO: 2160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160

TTTTGAACAC TATTTAACCC AGC

23

## 2) INFORMATION FOR SEQ ID NO: 2161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161

GATTTAACTT ATCCCAATAA CCT

23

## 2) INFORMATION FOR SEQ ID NO: 2162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

1113

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (C) ACCESSION NUMBER: X02166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162

ATGACTTTA	ATATTATCAA	ATTAGAAAAT	TGGGATAGAA	AAGAATATT	50
TGAACACTAT	TTTAACCAGC	AAACTACGTA	TAGCATTACT	AAAGAAATTG	100
ATATTACTTT	GTAAAGAT	ATGATAAAAAA	AGAAAGGATA	TGAAATT	150
CCTTCTTG	TTTATGCAAT	TATGGAAGTT	GTAAATAAAA	ATAAAGTGT	200
TAGAACAGGA	ATTAATAGTG	AGAATAAATT	AGGTTATTGG	GATAAGTTAA	250
ATCCTTGT	TACAGTTTT	AATAAGCAAA	CTGAAAATT	TACTAACATT	300
TGGACTGAAT	CTGATAACAA	CTTCACCTCT	TTTTATAATA	ATTATAAAAAA	350
TGACTTGCTT	GAATATAAAG	ATAAAGAAGA	AATGTTTCCT	AAAAAACCGA	400
TACCTGAAA	CACCATAACCG	ATTCAATGA	TTCCTTGAT	TGATTTAGT	450
TCATTTAATT	TAAACATTGG	TAACAATAGC	AACTTTTAT	TGCCTATTAT	500
TACGATAGGT	AAATTTATA	GTGAGAATAA	AAAATTAT	ATACCAGTTG	550
CTTGCAGCT	TCATCATGCT	GTATGTGATG	GTTACCATGC	TTCATTATT	600
ATGAATGAAT	TTCAAGATAT	AATTCTATAAG	GTAGATGATT	GGATT	648

2) INFORMATION FOR SEQ ID NO: 2163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163

ACCTTCATCC TACCGATGTG GGTT

24

2) INFORMATION FOR SEQ ID NO: 2164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164

CAACGACACC AGCACTGCCA TTG

23

2) INFORMATION FOR SEQ ID NO: 2165

1114

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella typhimurium*
- (B) STRAIN: H3380
- (C) ACCESSION NUMBER: AF071555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165

ATGACCACCA	CACGCCCGC	GTGGGCCTAT	ACGCTGCCGG	CAGCACTGCT	50
GCTGATGGCT	CCTTCGACA	TCCTCGCTTC	ACTGGCGATG	GATATTATC	100
TCCCTGTCGT	TCCAGCGATG	CCCGGCATCC	TGAACACGAC	GCCCGCTATG	150
ATCCAACCTCA	CGTTGAGCCT	CTATATGGTG	ATGCTCGGCG	TGGGCCAAGT	200
GATTTTGTT	CCGCTCTCAG	ACAGAACCGG	GCGACGGCCA	ATTCTACTTG	250
CGGGCGCAAC	GGCTTCGTC	ATTGCGTCTC	TGGGAGCAGC	TTGGTCTTCA	300
ACTGCACCGG	CCTTTGTCGC	TTTCCGCTCA	CTTCAAGCAG	TGGGCGCGTC	350
GGCCATGCTG	GTGGCGACGT	TCGCGACGGT	TCGCGACGTT	TATGCCAAC	400
GTCCTGAGGG	TGTCGTCA	TACGGCCTT	TCAGTTCGAT	GCTGGCGTTC	450
GTGCCTGCGC	TCGGCCCTAT	CGCCGGAGCA	TTGATCGGCG	AGTTCTTGGG	500
ATGGCAGGCG	ATATTCA	CTTGGCTAT	ACTGGCGATG	CTCGCACTCC	550
TAAATGCGGG	TTTCAGGTGG	CACGAAACCC	GCCCTCTGGA	TCAAGTCAAG	600
ACGCGCCGAT	CTGTCTTGCC	GATCTCGCG	AGTCCGGCTT	TTTGGGTTA	650
CACTGTCGGC	TTTAGCGCCG	GTATGGGCAC	CTTCTTCGTC	TTCTTCTCGA	700
CGGCTCCCCG	TGTGCTCATA	GGCCAAGCGG	AATATTCCGA	GATCGGATT	750
AGCTTGCGCT	TCGCCACTGT	CGCGCTTGTA	ATGATCGTGA	CAACCCGTT	800
CGCGAAGTCC	TTTGTGTCGA	GATGGGGCAT	CGCAGGATGC	GTGGCGCGTG	850
GGATGGCGTT	GCTTGTGTTGC	GGAGCGGTCC	TGTTGGGAT	CGGCGAAC	900
TACGGCTCGC	CGTCATTCT	CACCTTCATC	CTACCGATGT	GGGTTGTCGC	950
GGTCGGTATT	GTCTTCACGG	TGTCCGTTAC	CGCGAACGGC	GCTTGGCAG	1000
AGTCGACGA	CATCGCGGGA	TCAGCGGTG	CGTTCTACTT	CTGCATCAA	1050
AGCCTGATAG	TCAGTATCGT	CGGGACATTG	GCGGTGACGC	TGTTAAC	1100
CGATACAGCG	TGGCCCGTGA	TTTGTACGC	CACGGCAATG	GCAGTGCTGG	1150
TGTCGTTGGG	GCTGGCGCTC	CTTCGATCCC	GTGATGCTGC	CACCGAGAAG	1200
TCGCCAGTCG	TCTAG				1215

## 2) INFORMATION FOR SEQ ID NO: 2166

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166

GACAAACCAT TCCTGCTG

1115

18

## 2) INFORMATION FOR SEQ ID NO: 2167

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167

CAGCAGCTGG GCGGCGGT

18

## 2) INFORMATION FOR SEQ ID NO: 2168

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168

CATCAAAGTT GGTGAAGAAG TTG

23

## 2) INFORMATION FOR SEQ ID NO: 2169

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169

CCCGTTGCG AAAGGTGG

18

## 2) INFORMATION FOR SEQ ID NO: 2170

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Single

1116

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170

ACGTGACGTT GACAAACCA

19

2) INFORMATION FOR SEQ ID NO: 2171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171

TCGTTGGATT AACTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 2172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172

GTGTTGAAAT GTTCCGTAAA

20

2) INFORMATION FOR SEQ ID NO: 2173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173

AAGAAAAAAAT CTTCGAACTG GCTA

24

2) INFORMATION FOR SEQ ID NO: 2174

1117

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174

TCTACACGGC CGGTG

15

2) INFORMATION FOR SEQ ID NO: 2175

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175

CCGCCATACC CCGTTT

16

2) INFORMATION FOR SEQ ID NO: 2176

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176

CGGCATTACC ATTTCCACAC CTTT

24

2) INFORMATION FOR SEQ ID NO: 2177

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 bases  
(B) TYPE: Nucleic acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177

GGCACGGACA AACCATTCCCT GCTGCCTATC GAAGACGTGT TCCCGTGCC

49

2) INFORMATION FOR SEQ ID NO: 2178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178

GGCACGACAA ACCATTCCCTG CTGCCTATCG AACGTGCC

38

2) INFORMATION FOR SEQ ID NO: 2179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179

GGCAGCTCTA CTTCCGTACC ACTGACGTAACCGGCTGCC

39

2) INFORMATION FOR SEQ ID NO: 2180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180

TTCGCCGGCG TGGGC

15

2) INFORMATION FOR SEQ ID NO: 2181

(i) SEQUENCE CHARACTERISTICS:

1119

- (A) LENGTH: 15 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181

AGCGCCACGC GCAGG

15

2) INFORMATION FOR SEQ ID NO: 2182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182

GCGCGCCAAC GACTTCTACC ACGAAATGGA AGAGTCGCGC GC

42

2) INFORMATION FOR SEQ ID NO: 2183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Alcaligenes faecalis* subsp. *faecalis*
- (B) STRAIN: ATCC 8750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183

TATCTTGGTT	WGCTCGGCCG	CTGACGGCCC	AATGCCTCAG	ACTCGCGAGC	50
ACATCCTGCT	GAGCCGTCAG	GTTGGCGTTC	CTTACATCAT	CGTGTTCCTG	100
AAACAAGGCCG	ACATGGTTGA	TGACGAAGAG	CTGATCGAAC	TGGTTGAAAT	150
GGAAGTCGC	GAGCTGTTGT	CCAAGTACGA	CTTCCCTGGC	GACGACACCC	200
CGATCATCAA	GGGTTCGGCC	AAACTGGCTC	TGGAAGGCGA	CGAAGGCCCA	250
CTGGGCAGCC	AAGCCGTTCT	GGCTCTGGCC	GAAGCGCTGG	ACAACATACAT	300
TCCTACGCCT	GAGCGTGCAG	TTGACGGTAC	GTTCTGTATG	CCTGTTGAAG	350
ACGTGTTCTC	GATCTCCGGC	CGTGGTACGG	TTGTGACCGG	TCGTATTGAG	400
CGCGGCATCA	TCAAGGTCGG	CGAAGAAATC	GAAATCGTGG	GTATCAAAGA	450
CACGGTCAAG	ACCATTGTA	CCGGCGTTGA	AATGTTCCGC	AAACTGCTGG	500
ACCAGGGCGA	AGCTGGCGAT	AACGTCGGTC	TGCTGCTGCG	TGGTACCAAG	550
CGTGAAGACG	TGGAACGTGG	TCAAGTTCTG	GCCAAGCCAG	GCTCGATCAA	600
GCCACACACT	GACTTCGACG	CCGAGGTGTA	CATTCTGTCC	AAAGAAGAAG	650
GTGGTCGTCA	CACTCCTTTC	TTCAAGGGCT	ACCGTCCTCA	GTTCTACTTC	700

1120

CGTACAACGT	ACGTGACCGG	CACCATCGAG	CTGCCAGAAG	ACAAGGAAAT	750
GGTTCTGCCA	GGGCACAAACA	TTTCGATGAA	AGTGTCCCTG	ATCGCTCCTA	800
TCGCCATGGA	AGAAGGT				817

## 2) INFORMATION FOR SEQ ID NO: 2184

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter coli*
- (B) STRAIN: ATCC 43479

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2184

TACAATTGAA	GTTGAAAGAT	CTATCGTGT	TCTTGATGGT	GCTGTTGC GG	50
TATTTTGTTC	AGTGGGTGGG	GTGCAGCCTC	AAAGTGAAAC	AGTTTGGAGA	100
CAAGCAAATA	AATATGGTGT	TCCAAGAATA	GTATTTGTA	ATAAAATGGA	150
TAGAATCGGT	GCAAATTCT	ACAATGTAGA	AGATCAAATT	CGCAAACCGTT	200
TAAAAGCTAA	TCCAGTTCCA	CTTCAAATTC	CAATCGGTGC	TGAGGATAAT	250
TTTAAAGGCG	TAATCGATCT	TGTAACATAG	AAAGCTTTAG	TTTGGGAAGA	300
TGATACTAAG	CCAACGGATT	ATGTAGAAAA	AGAAAATTCCA	GCTGAACCTTA	350
AAGAAAAGGC	AGAAGAATAT	CGCACAAAAA	TGATAGAACG	AGTTTCTGAA	400
ACTTCAGATG	AGTTGATGGA	AAAATATT	GGTGGAGAAG	AATTAAGCCT	450
TGAAGAGATT	AAAACAGGG	TTAAAGCAGG	ATGTTTAAGT	CTTCTATCG	500
TTCCTATGCT	TTGCGGTACA	GCGTTAAAAA	ATAAAGGGGT	TCAACCTTTG	550
CTTGATGCTG	TTGTTGGCTTA	TTTACCAAGCT	CCTGATGAAG	TTGCTAATAT	600
CAAAGGGGAA	TATGAAGACG	GCACAGAAAGT	TTCTGTA	TCAACTGATG	650
ATGGCGAATT	TGCAGGACTT	GCATTTAAA	TTATGACAGA	TCCATTGTA	700
GGACAACCTA	CTTTCGTGCG	TGTTTATCGT	GGATGTTAG	AAAGCGGTT	750
TTATGCTTAT	AACTCAACCA	AAGATAAAA	AGAAAGAATT	GGTCGTTGT	800
TAAAAATGCA	CTCTAATAAA	AGAGAAGAAA	TTAAAGTTCT	TTACGCAGGA	850
GAAATCGGTG	CAGTTGTTAGG	ACTTAAAGAT	ACTTTAACAG	GGGATACTCT	900
TGCAAGTGAA	AAAGATAAAG	TAATTCTGA	AAGAATGGAT	TTCCCAGACC	950
CAGTTATTTC	TGTTGCAGTA	GAMCCAAAAA	CTAAAGCAGA	TCAAGAAAAA	1000
ATGTCTATTG	CACTAAATAA	ATTAGCTCAA	GAAGATCCAA	GCTTTAGAGT	1050
TTCTACGGAT	GAAGAAAGTG	GTCAAACAT	CATTTCAGGT	ATGGGTGAAT	1100
TACACCTTGA	AATTATTGTT	GATCGTATGC	TTCGTGAATT	TAAAGTGGAA	1150
GCTGAAGTGG	GACAACCTCA	AGTTGCTTAT	CGTGAAACTA	TCAGAAAAAC	1200
TGTTGAGCAA	GAATACAAAT	ACGCTAACGA	ATCAGGCGGT	CGTGGTCAGT	1250
ATGGACATGT	ATTCTTACGC	CTTGAGCCAC	TTGAGCCAGG	AAGTGGATAC	1300
GAGTTTGT	ACGACATCAA	AGGTGGGTA	ATTCCAAAAG	AATATATTCC	1350
TGCAGTAGAT	AAGGGTGTTC	AAGAAGCATT	GCAAAATGGT	GTTTTAGCAG	1400
GTTATCCAGT	AGAAGATGTT	AAAGTAACG	TTTATGATGG	AAGTTATCAC	1450
GAGGTGGATT	CATCTGAGAT	GGCATTAAA	CTTGCTGCTT	CTATGGGATT	1500
TAAAGAGGGT	GCTAGAAAAG	CAGGTGCTGT	GATCTTAGAG	CCTATGATGA	1550
AAGTTGAAGT	AGAAACTCCT	GAAGATTACA	TGGGCATGT	TATTGGCGAT	1600
CTTAATAAGC	GTCGTGGTCA	AGTAAATAGC	ATGGATGAAA	GAGGTGGTAA	1650
TA					1652

## 2) INFORMATION FOR SEQ ID NO: 2185

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Succinivibrio dextrinosolvens*
- (B) STRAIN: ATCC 19716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185

GCTATTCTAG	TAGTAGCAGC	AACTGATGGT	CCTATGCCAC	AGACCCGTGA	50
GCACATCCTA	TTAGCACGTC	AGGTAGCGT	ACCATACATC	ATCGTATTCC	100
TAAACAAAGTG	CGATATGGTT	GACGACGAGG	AATTATTAGA	GTTAGTTGAG	150
ATGGACGTAC	GTGATCTATT	AAATCAGTAC	CAGTTCCAG	GCGACGACAC	200
TCCAATCATC	CGTGGTTCAAG	CACTAGGTGC	ATTAAACGGC	GAAGAGAAGT	250
GGAAAGAGGC	AATCTATCAG	TTAGCAGACA	CTCTAGATTC	ATACATTCCA	300
GAGCCAAAGC	GTGATATCGA	TGATCCATTTC	CTATTACCAA	TCGAAGATAT	350
CTTCTCAATC	TCAGGTCGTG	GTACTGTAGT	AACCAGGCCGT	GTAGAGCGTG	400
GTATTGTACA	CGTAGGTGAC	GAAGTTGAAA	TCGTTGGTAT	TCGTCCAACC	450
ACCAAGACCA	CTGTAACCTGG	CGTTGAAATG	TTCCGTAAGT	TACTAGACGA	500
AGGTCGTGCA	GGTGATAACG	TTGGTGTCT	ACTACGTGGT	ACCAAGCGTG	550
ATGAGGGTGA	GCGTGGTCAG	GTTCTAGCTG	CTCCAGGCAC	AATCACTCCA	600
CACACCAAGT	TCACTGGTCA	GGTTTACGTA	CTAAGCAAGG	ATGAAGGTGG	650
TCGTCACACT	CCATTCTTCA	AGGGCTACCG	TCCACAGTTC	TTCTTCCGTA	700
CAACCGATAT	TACCGGTTCT	ATCGATCTGA	AAGAGGGCGT	AGAGATGGTA	750
ATGCCAGGTG	ATAACACCGA	CATGACCGTA	ACCCTAATCC	ACCCAGTAGC	800
TATGGCTGAA	GGCGAGAGAT				820

## 2) INFORMATION FOR SEQ ID NO: 2186

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186

ACCGCCTCAA AGCAGAAAGTA TACGTATTAT CAAAAGACGC GCGT

44

## 2) INFORMATION FOR SEQ ID NO: 2187

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1612 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187

CAGTGGGTGG	GGTGCAGCCT	CAAAGTAAA	CAGTTGGAG	ACAAGCAAAT	50
AAATATGGTG	TTCCAAGAAT	AGTATTTGTA	AACAAAATGG	ATAGAATCGG	100
TGCAAATTTC	TACAATGTAG	AAGATCAAAT	TCGCAACCGT	TTAAAAGCTA	150
ATCCAGTTCC	ACTTCAAATT	CCAATCGGTG	CTGAGGATAA	TTTAAAGGC	200
GTAATCGATC	TTGTAACAT	GAAAGCTTA	GTTTGGGAAG	ATGATACTAA	250
GCCAACGGAT	TATGTAGAAA	AAGAAATTCC	AGCTGAACCT	AAAGAAAAGG	300
CAGAAGAATA	TCGCACAAAA	ATGATAGAAG	CAGTTTCTGA	AACTTCAGAT	350
GAGTTGATGG	AAAAATATT	AGGCGGAGAA	GAATTAAGCC	TTGAAGAGAT	400
TAAAACAGGG	ATTAAAGCAG	GATGTTAAG	TCTTTCTATC	GTTCCTATGC	450
TTTGCAGTAC	AGCGTTAAA	AATAAAGGGG	TTCAACCTTT	ACTTGATGCT	500
GTTGTGGCTT	ATTTACCAAGC	TCCTGATGAA	GTGGCAAATA	TCAAGGGTGA	550
ATATGAAGAT	GGCACAGAAG	TTTCTGTAAA	ATCAACTGAT	GATGGCGAGT	600
TTGCAGGACT	TGCATTTAAA	ATTATGACAG	ATCCATTGTT	AGGACAACTT	650
ACTTTCGTGC	GTGTTTATCG	CGGTTGTTA	GAAAGTGGTT	CTTATGCTTA	700
TAACTCAACT	AAAGATAAAA	AAGAAAGAAT	TGGTCGTTTG	TTAAAATGC	750
ACTCTAACCA	AAGAGAAAGAG	ATTAAAGTGC	TTTACGCAGG	CGAAATTGGT	800
GCTGTTGTTAG	GACTTAAAGA	TACTTTAAC	GGGGATACTC	TTGTAAGTGA	850
AAAAGATAAG	GTAATCCTTG	AAAGAATGGA	TTTCCAGAT	CCAGTTATT	900
CTGTTGCAGT	TGAGCCAAA	ACTAAAGCAG	ATCAAGAAAA	AATGTCTATT	950
GCTTTAAATA	AATTAGCACA	AGAAGATCCA	AGTTTTAGAG	TTTCTACAGA	1000
TGAAGAAAGT	GGCCAAACTA	TCATTTCAAG	TATGGGTGAG	TTACACCTTG	1050
AAATTATCGT	TGATAGAATG	CTTCGTGAAT	TTAAAGTTGA	AGCTGAAGTA	1100
GGTCAACCAC	AAGTTGCTTA	TCGCGAAACT	ATTAGAAAAA	CTGTTGAACA	1150
AGAATACAAA	TACGCTAAC	AATCAGGTGG	TCGTGGTCAG	TATGGACATG	1200
TATTCTTACG	CCTTGAACCA	CTTGAGCCAG	GTAGTGGATA	TGAATTGTT	1250
AATGATATCA	AAGGTGGAGT	AATTCCAAA	GAATACATTC	CTGCAGTTGA	1300
TAAAGGTGTT	CAAGAACAT	TACAAAATGG	TGTTTTAGCA	GGTTATCCTG	1350
TGGAAGATGT	TAAAGTAAC	GTTTATGATG	GAAGTTATCA	CGAGGTGGAT	1400
TCATCTGAGA	TGGCGTTAA	ACTTGCTGCT	TCTATGGGCT	TTAAAGAAGG	1450
TGCTAGAAAA	GCAGGTGCTG	TGATCTTAGA	GCCTATGATG	AAAGTTGAAG	1500
TAGAAACTCC	TGAAGATTAC	ATGGGTGATG	TTATTGGAGA	TCTTAACAAA	1550
CGCCGTGGTC	AAGTAAATAG	CATGGATGAG	CGTGGTGGAA	ATAAAATCAT	1600
CACAGCATT	TG				1612

## 2) INFORMATION FOR SEQ ID NO: 2188

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Campylobacter jejuni* subsp. *jejuni*
- (B) STRAIN: ATCC 33560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188

ACAATTGAAG	TTGAAAGATC	TATGCGTGT	CTTGATGGTG	CTGTTGCGGT	50
ATTTTGTCA	GTGGGTGGGG	TGCAGCCTCA	AAGTGAAACA	GTTTGGAGAC	100
AAGCAAATAA	ATATGGTGT	CCAAGAATAG	TATTTGTAAA	TAAAATGGAT	150
AGAATCGGTG	CAAATTCTA	CAATGTAGAA	GATCAAATTC	GCAACCGTT	200
AAAAGCTAAT	CCAGTTCCAC	TTCAAATTCC	AATTGGTGCT	GAGGATAATT	250
TTAAAGGCGT	AATCGATCTT	GTAACTATGA	AAGCTTTAGT	TTGGGAAGAT	300
GATACTAAGC	CAACGGATT	TGTAGAAAAA	GAAATTCCAG	CTGAACCTAA	350
AGAAAAGGCA	GAAGAATATC	GCACAAAAAT	GATAGAAGCA	GTTTCTGAAA	400
CTTCAGATGA	GTTGATGGAA	AAATATTAG	GCGGAGAAGA	ATTAAGCCTT	450
GAAGAGATTA	AAACAGGGAT	TAAAGCAGGA	TGTTTAAGTC	TTTCTATCGT	500
TCCTATGCTT	TGCGGTACAG	CGTTAAAAAA	TAAAGGGTT	CAACCTTTGC	550
TTGATGCTGT	TGTGGCTTAT	TTACCAGCTC	CTGATGAAGT	GGCAAATATC	600
AAGGGTGAAT	ATGAAGATGG	CACAGAAGTT	TCTGTAAAAT	CAACTGATGA	650
TGGCGAGTTT	GCAGGACTTG	CATTAAAAT	CATGACAGAT	CCATTGTTAG	700
GACAACTTAC	TTTCGTGCGT	GTTTATCGCG	GTTGTTAGA	AAGCGGTTCT	750
TATGCGTATA	ACTCAACTAA	AGATAAAAAA	GAAAGAATTG	GTCGTTTGT	800
AAAAATGCAC	TCTAACAAAA	GAGAAGAGAT	TAAAGTGT	TACGCAGGCG	850
AAATTGGTGC	TGTTGTAGGA	CTTAAAGATA	CTTAAACAGG	GGATACTCTT	900
GCAAGTAAA	AAGATAAGGT	AATCCTTGAA	AGAATGGATT	TTCCAGATCC	950
AGTTATTCT	GTTGCAGTTG	AGCCAAAAAC	TAAAGCTGAT	CAAGAAAAAA	1000
TGTCTATTGC	TTTAAATAAA	TTAGCACAAG	AAGATCCAAG	TTTAGAGTT	1050
TCTACAGATG	AAGAAAGTGG	TCAAACATTC	ATTTCAGGTA	TGGGTGAGTT	1100
ACACCTTGAA	ATTATCGTTG	ATAGAATGCT	TCGTGAATT	AAAGTTGAAG	1150
CTGAAGTAGG	TCAACCACAA	GTTGCTTATC	GCGAAACTAT	TAGAAAAACT	1200
GTTGAACAAG	AATACAAATA	CGCTAAACAA	TCAGGTGGTC	GTGGTCAGTA	1250
TGGACATGTA	TTCTTACGCC	TTGAACCAC	TGAGCCAGGT	AGTGGATATG	1300
AATTGTTAA	TGATATCAAA	GGTGGGGTAA	TTCCAAAAGA	ATACATTCT	1350
GCAGTTGATA	AAGGTGTTCA	AGAACGATTA	CAAAATGGTG	TTTAGCAGG	1400
TTATCCTGTG	GAAGATGTTA	AAGTAACTGT	TTATGATGGA	AGTTATCACG	1450
AGGTGGATT	ATCTGAGATG	GCGTTAAC	TTGCTGCTTC	TATGGGCTTT	1500
AAAGAAGGTG	CTAGAAAAGC	AGGCCTGTG	ATCTTAGAGC	CTATGATGAA	1550
AGTTGAAGTA	GAAACTCCTG	AAGATTATAT	GGGTGATGTT	ATTGGAGATC	1600
TTAACAAACG	CCGTGGTCAA	GTAAATAGCA	TGGATGAGCG	TGGTGGAAAT	1650
AAAATCATCA	CAGCATT				1667

2) INFORMATION FOR SEQ ID NO: 2189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1255 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania guyanensis*  
 (B) STRAIN: ATCC 50126

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189

TGACGGCGCT	GGACGTGACG	GAGGACCTCG	GCCGCGATGA	GCCGCTGACG	50
CTGGAGATCG	TGCAGCACTT	GGATGCGAAC	ACCGGCCGCT	GCATTGCGAT	100
GCAGACGACG	GACCTGCTGA	AGCTGAAGTC	GAAGGTTGTG	TCGACCGGGCG	150
GCAACATCTC	CGTGCCGGTG	GGCCGCGAGA	CACTGGGCCG	CATCTTCAAC	200
GTGCTGGCG	ACGCGATTGA	CCACCGCGGC	CCCGTGTGCG	AGAAGATGCG	250
CATGGCGATC	CACGCCGAGG	CGCCGAAGCT	GGCGGACCAG	GCTGCGGAGG	300
ACACGATCCT	GACGACCGGC	ATCAAGGTGA	TCGACCTGAT	TCTGCCCTAC	350
TGCAAGGGCG	GCAAGATCGG	CCTGTTCGGC	GGTGCCGGTG	TGGGCAAGAC	400
TGTGATCATC	ATGGAGCTGA	TCAACAAACGT	CGCGAAGGGG	CACGGCGGCT	450
TCTCCGTGTT	CGCCGGCGTT	GGCGAGCGCA	CGCGCGAGGG	CACGGACCTG	500
TACCTGGAGA	TGATGCAGTC	AAAGGTGATT	GACCTGAAGG	GCGAGTCGAA	550
GTGCGTGCTT	GTGTACGGGC	AGATGAACGA	GCCCCCGGGT	GCGCGCGCGC	600
GCCTTGCGCA	GTCTGCGCTG	ACGATGGCG	AGTACTTCCG	CGACGTGGAG	650
GGCCAGAACG	TGCTGCTGTT	CATCGACAAC	ATCTTCCGCT	TCACGCAGGC	700
GAACCTCCGAG	GTGTCTGCGC	TGCTGGGCCG	CATCCCCGGCC	GCCGTGGGTT	750
ACCAGCCGAC	GCTTGCGGAG	GATCTTGCA	TGCTGCAGGA	GCGCATTACG	800
TCGACGACGA	AGGGATCGAT	TACGTCTGTG	CAGGCTGTGT	ACGTGCCTGC	850
GGATGATATC	ACGGACCCCG	CGCCCGCGAC	GACGTTCTCG	CACCTGGACG	900
CGACGACTGT	GCTGGACCGC	GCGGTGGCGG	AGTCGGGCAT	CTACCCCTGCC	950
GTGAACCCGC	TGGAGTGCAG	GTCGCGCATC	ATGGACCCCG	ATGTGATCGA	1000
CGTGGACCAT	TACAACGTTG	CACAGGATAT	CGTCCAGATG	CTGACCAAGT	1050
ACAAGGAGCT	GCAGGACATC	ATTGCGGTGC	TTGGCATCGA	CGAGCTGAGC	1100
GAGGAGGACA	AGGTCGTGGT	GGACCGCGCG	CGCAAGGTGA	CGCGGTTCCCT	1150
GTCGCAGCCG	TTCCAGGTTG	CGGAGGTGTT	CACCGGCATG	ACGGGCCACT	1200
ACGTGCAGCT	GAGCGACACG	GTGGAGTCGT	TCTCTGGCCT	GCTGATGGGG	1250
TCGTA					1255

## 2) INFORMATION FOR SEQ ID NO: 2190

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1248 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Trypanosoma brucei* subsp. *brucei*  
 (B) STRAIN: EATRO 795

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190

GCCCTTGACG	TTGTTGACAA	ACTTGGCCGT	GATGAGCCTC	TTACTCTTGA	50
GATCGTGCAG	CATCTTGACG	CCCACACGGG	CCGCTGTATC	GCGATGCAA	100
CGACGGATCT	CCTCAAAC TG	AAGGCAAAGG	TCGTTTCGAC	AGGTGGCAAC	150
ATTTCCGTTG	CTGTCGGCCG	GGAAACACTA	GGTCGTATCT	TCAACGTGCT	200
TGGAGACGCT	ATTGACCAAGC	GCGGCCCCGT	TGGTGAGAAA	CTGCGCATGC	250
CCATCCATGC	CGTGGCTCCC	AAGCTTGCGG	ACCAGGCCGC	TGAGGATGCG	300
GTGCTCACAA	CTGGTATTAA	GGTGATTGAT	CTCATTCTCC	CTTACTGCAA	350

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AGGTGGAAAA	ATTGGCCTCT	TTGGGGGTGC	GGGTGTGGGC	AAAACCGTCA	400
TTATTATGGA	GCTCATTAAC	AACGTTGCCA	AGGGTCACGG	TGGTTTCTCT	450
GTCTTCGCTG	GTGTTGGTGA	GCGTACCCGT	GAGGGAACGG	ATTGTATCT	500
TGAGATGATG	CAGTCTAAGG	TTATTGACCT	TAAGGGTGAG	TCCAAATGTG	550
TGTTGGTGTG	CGGTCAAGATG	AACGAGCCCC	CAGGTGCCCG	TGCCGCTGTT	600
GCGCAGTCGG	CTCTGACGGAT	GGCTGAGTAC	TTCCGTGATG	TGGAGGGCCA	650
AGATGTGCTT	CTTTTTATCG	ACAATATTTC	TCGTTTCACT	CAGGCTAACT	700
CCGAGGTGTC	GGCGCTTCTG	GGTCGTATTC	CCGCCGCTGT	TGGCTACCAAG	750
CCTACCCCTCG	CTGAGGATCT	AGGGCAGTTG	CAGGAGCGTA	TTACCTCAAC	800
AACGAAAGGC	TCCATTACTT	CTGTGCAGGC	CGTATACGTG	CCGGCCGATG	850
ACATTACCGA	TCCAGCTCCA	GCAACAAACCT	TCTCACATCT	GGACGCCACA	900
ACTGTGTTGG	ACCGTGCTGT	TGCCGAGTCT	GGTATCTACC	CCGCTGTTAA	950
CCCACTGGAA	TGCGCCTCGC	GTATCATGGA	CCCCGACGTT	ATCAGTGTGG	1000
ATCACTACAA	TGTTGCACAA	GATGTGGTAC	AGATGCTCAC	CAAGTACAGG	1050
GAATTACAGG	ATATCATTGC	TGTCCTTGGT	ATCGACGAGC	TAAGCGAGGA	1100
GGACAAACTT	ATCGTGGACC	GTGCGCGTAA	GTTGGTGAAG	TTCCCTCTCCC	1150
AGCCATTCCA	AGTTGCTGAG	GTCTTCACAG	GAATGACTGG	CCATTACGTG	1200
CAGTTGGATG	ACACCATCGA	TTCCCTTTCT	GGTCTCCTCA	TGGGTACG	1248

## 2) INFORMATION FOR SEQ ID NO: 2191

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aspergillus nidulans*
- (B) STRAIN: WSA-176

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191

GAGCTGATTG	TAAGTCATCG	ACCACTTGAT	ATATGAATAC	ATCTAACAGT	50
AGTAGAACAA	CATCGCCAAG	GCTCACGGTG	GTTACTCCGT	CTTCACTGGT	100
GTCGGTGAGC	GTACTCGTGA	GGGTAACGAT	CTGTACCACG	AAATGCAGGA	150
GACTGGTGTG	ATTCACTCG	ACGGCGAACATC	CAAGGTGTCT	CTTGTGTTCG	200
GTCAGATGAA	CGAGCCCCCA	GGTGTCTCGT	CCCGTGTCGC	CCTTACTGGT	250
CTGACCATCG	CCGAATACTT	CCGTGACGGAG	GAGGGTCAGG	ACGTGCTGCT	300
CTTCATTGAC	AACATTTTCC	GTTCACCCA	GGCCGGTTCC	GAGGTGTCTG	350
CCCTTCTTGG	TCGTATCCCC	TCTGCCGTG	GTTACCAAGCC	CACTCTGGCC	400
GTCGACATGG	GTGGTATGCA	GGAACGTATT	ACCACCAACCA		440

## 2) INFORMATION FOR SEQ ID NO: 2192

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1262 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Leishmania panamensis*  
 (B) STRAIN: ATCC 50158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192

GCTGACGGCG	CTGGACGTGA	CGGAGGACCT	CGGCCGCGAT	GAGCCGCTGA	50
CGCTGGAGAT	CGTGCAGCAC	TTGGATGCGA	ACACCGGCCG	CTGCATTGCG	100
ATGCAGACGA	CGGACCTGCT	GAAGCTGAAG	TCGAAGGTTG	TGTCGACCGG	150
CGGCAACATC	TCCGTGCCGG	TGGGCCGCGA	GACGCTGGGC	CGCATCTTCA	200
ACGTGCTGGG	CGACGCGATT	GACCACCGCG	GCCCCGTGTG	CGAGAAGATG	250
CGCATGGCGA	TCCACGCCGA	GGCGCCGAAG	CTGGCGGACC	AGGCTGCGGA	300
GGACACGATC	CTGACGACCG	GCATCAAGGT	GATCGACCTG	ATTCTGCCCT	350
ACTGCAAGGG	CGGCAAGATC	GGCCTGTTCG	GCGGTGCCGG	TGTGGGCAAG	400
ACTGTGATCA	TCATGGAGCT	GATCAACAAC	GTCGCGAAGG	GGCACGGCGG	450
CTTCTCCGTG	TTCGCCGGCG	TTGGCGAGCG	CACGCGCGAG	GGCACGGACC	500
TGTACCTGGA	GATGATGCAG	TCAAAGGTGA	TTGACCTGAA	GGCGAGTCG	550
AAGTGCCTGC	TTGTGTACGG	GCAGATGAAC	GAGCCCCCGG	GTGCGCGCGC	600
GCGCGTTGCG	CAGTCTGCGC	TGACGATGGC	CGAGTACTTC	CGCGACGTGG	650
AGGGCCAGAA	CGTGCTGCTG	TTCATCGACA	ACATCTTCCG	CTTCACGCAG	700
GCGAACTCCG	AGGTGTCTGC	GCTGCTGGGC	CGCATCCCGG	CCGCCGTGGG	750
TTACCAGCCG	ACGCTTGCAG	AGGATCTTGG	CATGCTGCAG	GAGCGCATT	800
CGTCGACGAC	GAAGGGATCG	ATTACGTCG	TGCAAGGCTGT	GTACGTGCCT	850
GCGGATGATA	TCACGGACCC	CGCGCCCGCG	ACGACGTTCT	CGCACCTGG	900
CGCGACCGACT	GTGCTGGACC	GCGCGGTGGC	GGAGTCGGGC	ATCTACCCCTG	950
CCGTGAACCC	GCTGGAGTGC	GCGTCGCGCA	TCATGGACCC	CGATGTGATC	1000
GACGTGGACC	ATTACAACGT	TGCACAGGAT	ATCGTCCAGA	TGCTGACCAA	1050
GTACAAGGAG	CTGCAGGACA	TCATTGCGGT	GCTTGGCATC	GACGAGCTGA	1100
GCGAGGAGGA	CAAGGTCTGT	GTGGACCGCG	CGCGCAAGGT	GACGCGGTT	1150
CTGTCGCAGC	CGTTCCAGGT	TGCGGAGGTG	TTCACCGGCA	TGACGGGCCA	1200
CTACGTGCAG	CTGAGCGACA	CGGTGGAGTC	GTTCTCTGGC	CTGCTGATGG	1250
GGTCGTACGA	CC				1262

2) INFORMATION FOR SEQ ID NO: 2193

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 912 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Aspergillus nidulans*  
 (B) STRAIN: WSA-176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193

TTCCGATGGT	CAAATGTACG	ATTGATATTG	CTTCCAGGCCA	GTCAGGATAA	50
CAGCTGATAC	CAGTTGAAA	TAGGCCCGAG	ACTCGTGAGC	ACTTGTGTTG	100
TGCCCGTCAG	GTTGGTGTCC	AGAAGATCGT	TGTCTTCGTC	AACAAGGTTG	150
ACGCTGTCGA	TGACCCCTGAG	ATGTTGGAGC	TTGTTGAGCT	CGAGATGCGT	200

GAGCTCCTCA	ACACTTACGG	TTTCGAGGGA	GAGGAGACCC	CTATCATCTT	250
CGGTTCCGCC	CTGTGCGCTC	TCGAAGGCCG	CCGCGAGGAC	ATTGGTACTC	300
AGCGTATTGA	CTCCCTCCTC	GAGGCCGTTG	ACACATTGGAT	CCCTACCCCC	350
CAGCGTGA	TGGACAAGCC	CTTCCTGATG	TCCATTGAGG	AAGTTTCTC	400
CATTGGTGGT	CGTGGTACCG	TCGCCTCTGG	TCGTGTCGAG	CGTGGTCTCC	450
TCAAGAAGGA	TACCGAAGTT	GAAATTCAAG	GTGCTGATGG	TATTCTGAAG	500
ACCAAGGTCA	CCGACATTGA	GACCTTCAAG	AAGAGCTGCG	ATGAGTCTCG	550
TGCTGGTGAC	AACTCCGGTC	TTCTCCTCCG	TGGTATCCGT	CGTGAGGATG	600
TTCGTCGTGG	TATGGTCATC	GCTGCCCCCTG	GCTCCATCAA	GGCCTCCAAG	650
AAGTTCATGG	TCTCCATGTA	CGTCTTGACT	GAGGCTGAAG	GTGGCCGCAA	700
GAACGGCTTC	GGTGCCAAC	ACCGCCCCCA	GGCTTCATC	CGCACTGCTG	750
GTAAGTTTCG	AACTATTGA	TTCATTGATC	ACGTCCCTAA	CTGTTACTTT	800
AGACGAGGCT	TGCGACCTTC	ATTCCCTGA	TGAGGCGAC	AAGGACCGCC	850
ACGTCAATGCC	CGGTGACAAC	GTCGAAATGG	TCCTCAACCT	CAACAACCCC	900
GTGCTGCTG	AG				912

## 2) INFORMATION FOR SEQ ID NO: 2194

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 887 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aureobasidium pullulans*
- (B) STRAIN: WSA-234

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194

TCATCGTCGT	CGCCGCTTCT	GACGGTCAGA	TGCCCCAGAC	CAGAGAGCAC	50
TTGCTTCTCG	CCC GTCAAGGT	CGGTATCCAG	AAGATTGTCG	TCTTCGTCAA	100
CAAGGTGAC	GCCATCGAGG	ACAAGGAGAT	GCTTGAGCTC	GTGGAGATGG	150
AGATGCGTGA	GCTCCTCAGC	AGCTACGGCT	TCGAGGGTGA	CGAGACCCCC	200
ATCGTCATGG	GTTCCGCTCT	TTGTGCCCTT	GAGAACCGCC	AGCCCGAGAT	250
TGGAACCAACC	CAGATCGACA	ACCTGATGAA	CGCTGTCGAC	GAGTGGATCC	300
CCACTCCCCA	GAGAGATCTT	GAGAACCCCT	TCCTCATGTC	CGTTGAGGAT	350
GTCTTCTCTA	TCCCCGGTCG	TGGTACTGTC	GTTCCTGGCC	GTGTTGAGCG	400
TGGTACCCCTG	AAGAAGGATT	CCGAAATCGA	GCTTGTCGGC	AAGAACAAAGG	450
TCCCCATCAA	GACCAAGGTC	ACCGACATCG	AGACCTTCAA	GAAGTCTTGC	500
GACGAGTCCC	GCGCTGGTGA	CAACTCCGGT	CTTCTGCTCC	GTGGTATCAA	550
GCGTGAGGAT	GTCAACCGTG	GTATGGTTGT	CGTCAAGCCC	GGTACCGTCA	600
CCTCGCACAA	GAAGTTCCCTC	GTCTCCATGT	ACGTCCCTGAC	CAAGGAGGAG	650
GGTGGTCGTC	ACACTGGTTT	CCACGGAAAC	TACCGTCCCC	AGATCTTCAT	700
CCGTACCGCT	GGTAAGTCCT	GACTTTGAAC	TGCTGACCAA	TTTCGACATC	750
TCTAACATGT	TTTACAGACG	AGGCTGCCGC	TATTGACTGG	CCCGAAGGCA	800
CCGAGGACGC	TGACTCCAAG	ATGGTCATGC	CCGGTGACAA	CGTCGAGATG	850
GTCTGCTCTC	TTCACAGACC	TCTTGCCGTT	GAACAGG		887

## 2) INFORMATION FOR SEQ ID NO: 2195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Emmonsia parva*
- (B) STRAIN: ATCC 10784

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195

TGACGGCCAA	ATGTAGGACT	CTTGCAGCGG	ACTGACTGAT	TGGGGGAAAT	50
CCATTTTTTC	TTTTTTCTTT	TTCTTTTTGA	GTACATGATT	ATACTAATAT	100
TTGGATAACG	TACCAGGCCT	CAAACACGTG	AACATTTACT	CCTTGCCCGA	150
CAAGTCGGTG	TCCAGAAAGAT	CGTCGTTTC	GTAAACAAGG	TCGATGTTCT	200
CGAAGATAAG	GAGATGTTGG	AGCTTGTGCA	GTTGGAATG	AGAGAGCTCT	250
TGAACACCTA	CGGATTGAG	GGTGAGGAAA	CGCCCATCAT	CTTCGGTTCT	300
GCCCTTGTG	CCATGGAGGG	CCCGGAGCCT	GAGCTGGCG	AGAAGAGAAT	350
TGATGAATTG	CTCGACGCTG	TTGATAGCTG	GATCCCTACG	CCGCAACGTG	400
ATACGGAAAA	ACCCTTCCTA	ATGTCCATTG	AGGAAGTGT	CTCCATCTCC	450
GGTCGTGGAA	CCGTTGCTC	CGGCCGTGTT	GAGCGTGGTG	TCCTCAAGAA	500
GGATTCCGAA	GTCGAGCTTG	TTGGCGCGG	CGTCGCCCA	ATCAGGACCA	550
AGGTAACCGA	TATCGAAACC	TTCAAGAAGT	CCTGCGACGA	GTCCAGGGCT	600
GGAGACAAC	CTGGCCTTT	GTTGCGTGGT	GTCAGCGTG	AGGATATCCG	650
CCGTGGTATG	GTCGTTGTCG	TTCCTGGCAG	CGTCAAGGCC	CACGACAAGT	700
TCTTGGTGTC	CATGTATGTT	CTGACCGAAG	CCGAGGGTGG	TCGCCGAAC	750
GGATTCCGCC	AAAATATCG	TCCTCAAATG	TTTATCCGCA	CAGCTGGTAC	800
GTAACGTATA	ATGCCTCTCC	TCTTCATATA	TACCACCCCC	CCCACCACTG	850
ACTCCCTGAC	TCTTCGATTA	CAGACGAGGC	CGCCGATCTC	AGCTTCCCTG	900
ACGCAGCAGA	CGAAACCAAA	CTGGTTATGC	CCGGTGACAA	CGTCGAGATG	950
ATCCTCAAGA	CACACCGCCC	CATAGCTGCC	GAAAG		984

## 2) INFORMATION FOR SEQ ID NO: 2196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Exserohilum rostratum*
- (B) STRAIN: WSA-215

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196

GCCGCCTCTG	ACGGCCAAAT	GCCCCAGACC	CGTGAGCACT	TGCTGCTTGC	50
TCGCCAGGTC	GGTGTTCAGA	AGATTGTTGT	TTTGTCAAC	AAGGTCGATG	100
CCGTCGAGGA	CAAGGAGATG	TTGGAGCTCG	TTGAGATGGA	GATGCGTGAG	150
TTGCTCAGCA	GCTATGGCTT	CGAGGGCGAT	GAGACTCCCA	TTGTCATGGG	200

CTCCGCTCTC	TGCGCCATCG	AGGGCCGTGA	GCCCGAAATT	GGTGTCAACC	250
GTATTGATGA	GCTGCTCGAG	GCTGTCGACA	CCTGGATCCC	CACCCCTCAG	300
CGTGATACCG	ACAAGCCCTT	CCTCATGGCT	GTTGAGGACG	TCTTCTCCAT	350
TGCTGGCCGT	GGTACCGTCG	TTTCTGGCCG	TGTCGAGCGA	GGTGTCTTGA	400
AGCGCGATGC	CGAAGTCGAG	CTGGTTGGCA	AGGGCACTGC	GCCCATCAAG	450
ACCAAGGTAA	CCGACATTGA	AACCTTCAAG	AAGTCGTGTG	AAGAGTCTCG	500
CGCCGGTGAC	AACTCGGGTC	TCCCTCCTCCG	TGGTGTCAAG	CGTGACGACG	550
TCCGCCGTGG	CATGGTCGTT	TCTGTTCCCTG	GACAAGTCAA	GGCCCACAAAG	600
AAGTTCCCTCG	TCTCCATGTA	TGTGTTGAGC	AAAGAGGAAG	GTGGCCGCCA	650
CACGGGCTTC	GGCGAGAACT	ACAGGCCACA	AATGTTCATC	CGTACTGCTG	700
ACGAGTCATG	CGCGCTGCAC	TGGCCAGAAG	GTACCCCAGA	TGCTCACGAC	750
AAGCTTGTAA	TGCCTGGTGA	TAACGTTGAG	ATGGTTGTG	AGCTTCACGT	800
	GCCACA				806

## 2) INFORMATION FOR SEQ ID NO: 2197

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Fusarium moniliforme*
- (B) STRAIN: WSA-213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197

ACCCGTGAAC	ACTTGCTCCT	CGCTCGTCAG	GTTGGTGTTC	AGCGAATTGT	50
CGTCTTGTG	AACAAGGTG	ATGCCATTGA	TGACCCCGAG	ATGCTTGAGC	100
TCGTCGAGAT	GGAGATGCGC	GAGCTTCTTA	ACACCTATGG	CTTCGAAGGC	150
GACGACACTC	CCGTCATCAT	GGGCTCGGCT	CTCATGTCTC	TCCAGAACCA	200
GCGCCCTGAG	ATTGGCACCG	AGAAGATTGA	TGAGCTTCTT	GCTGCCGTCG	250
ACGAGTGGAT	CCCAACCCCC	GAGCGTGACC	TTGACAAGCC	CTTCCTTATG	300
TCCGTGAGG	ATGTCTTCTC	CATTGCTGGC	CGTGGTACCG	TCGTGTCTGG	350
CCGTGTGGAG	CGTGGTGTTC	TGAAGCGTGA	CCAGGAGATC	GAGCTTGTG	400
GAAAGGGTCA	GGAGGTTATC	AAGACCAAGG	TTACCGACAT	CGAGACCTTC	450
AAGAAAGTCTT	GTGAGCAGTC	CCAGGCTGGT	GACAACCTCTG	GTCTCCTCAT	500
CCGAGGTGTT	CGCCGTGAGG	ATGTCCGCCG	TGGTATGGTC	GTCTGCGCTC	550
CTGGCACCGT	GAAGTCTCAC	ACCCAGTTCC	TGCTTCCCT	CTATGTCCCTC	600
TCCAAGGAGG	AGGGTGGCCG	ACACACCGGT	TTCCAGGAGC	ACTACCGACCC	650
CCAGCTCTAC	CTCCGAACCG	CAGATGAGTC	CATTGACCTG	ACTTTCCCTG	700
AGGGTACTGA	GGATGCCTCC	AGCAAGATGG	TCATGCCTGG	CGACAAACACC	750
GAGATGGTTG	TCACCATGGG	TCACCCCAAT	GCCATCGAGG	TTGGTCAGC	799

## 2) INFORMATION FOR SEQ ID NO: 2198

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 bases
- (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Fusarium solani*  
 (B) STRAIN: ATCC 32793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198

CTCTGACGGT	CAGATGCCCC	AGACCCGTGA	GCACTTGCTG	CTTGCCCGTC	50
AGGTCGGTGT	CCAGAAAGATT	GTCGTCTTCG	TCAACAAAGGT	CGATGCCATT	100
GACGACCCCTG	AGATGCTTGA	GCTCGTCGAG	ATGGAGATGC	GTGAGCTCCT	150
CAACACCTAC	GGCTTCGAGG	GTGACGAGAC	CCCTGTCATC	ATGGGCTCTG	200
CTCTCATGTC	CCTCCAGAAC	CAGCGCCCCG	AGATCGGTAG	CCAGAAAGATT	250
GACGAGCTCC	TTGCCGCCGT	TGACGAGTGG	ATCCCTACCC	CCGAGCGTGA	300
CCTTGACAAG	CCCTTCCTCA	TGTCCGTTGA	GGATGTCTTC	TCCATTGCCG	350
GCCGTGGTAC	CGTCGTCTCT	GGCCGTGTCG	AGCGTGGTGT	CCTGAAGCGC	400
GACCAGGAGA	TTGAGCTCGT	CGGCAAGGGT	AACGAGGTCA	TCAAGACCAA	450
GGTCACCGAC	ATTGAGACCT	TCAAGAAGTC	TTGCGAGCAG	TCCCAGGCTG	500
GTGACAACTC	TGGTCTCCTC	ATCCGAGGTG	TCCGCCGTGA	GGATGTCCGC	550
CGTGGTATGG	TCGTCTGCGC	CCCCGGCACT	GTCAAGTCCC	ACACTCAGTT	600
CCTTTCTTCC	CTCTACGTCC	TCACCAAGGA	GGAGGGTGGC	CGACACACTG	650
GCTTCCAGGA	GCACTACCGA	CCCCAGCTCT	ACCTCCGAAC	TGCTGATGAG	700
TCCATCGACC	TGACCTTCCC	CGAGGGTACC	GAGGACGCCA	GCAGCAAGAT	750
GGTCATGCC	GGTGACAACA	CCGAGATGGT	CATCACCATG	GGCCACCCCA	800
ACGCCATTGA	GGTCGGTCA				819

2) INFORMATION FOR SEQ ID NO: 2199

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1025 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Histoplasma capsulatum*  
 (B) STRAIN: WSA-377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199

TGCTGACGGC	CAAATGTAAG	ACGCCCGAG	GGAGTGCTGA	AGGTTTTATG	50
CTTTTTAGGC	CCTTTGTTTC	TGAGAGCATG	ATGATACTAA	TACTCGGAAA	100
CGTATCTATT	AGGCCTAAA	CACGTGAGCA	TTTGCTCCTT	GCCCACAGG	150
TCGGTGTCCA	AAAGATCGTC	TTTTCTGTGA	ACAAAGTCGA	CGCCCTTGAG	200
GACAAGGAGA	TGTTGGAGCT	TGTCGAGTTA	GAAATGAGAG	AGCTCTTAAA	250
CACCTACCGA	TTTGAGGGTG	AAGAGACACC	CATCATCTT	GGTTCTGCC	300
TTTGCGCCAT	GGAAGGCCGT	GAGCCTGAGT	TGGGAGAAAA	GAAAATTGAT	350
GAATTGCTGG	AGGCTGTTGA	TACTTGGATC	CCAACACCCAC	AACGTGATAC	400
CGAAAAACCT	TTCTTGATGT	CCGTTGAGGA	AGTATTCTCT	ATCTCCGGTC	450
GTGGAACCGT	TGCCTCCGGT	CGTGTGAGC	GCGGTGTCT	CAAGAAGGAT	500

TCAGAACGTCG	AGCTAATTGG	GGCGGGCTCC	ACCCCCATCA	GGACGAAGGT	550
AACTGATATC	GAAACTTCA	AGAAATCCTG	TGACGAGTCT	AGAGCTGGGG	600
ACAACTCCGG	TCTTTATTG	CGTGGTATCA	AGCGTGAAGA	TATCCGCCGT	650
GGTATGGTAG	TTGCCGTTCC	TGGCAGCGTC	AAGGCCACG	ACAAGTTCTT	700
GGTGTGATG	TATGTCCTGA	CCGAAGCTGA	GGGTGGTCGC	CGAACCGGAT	750
TCGGCCAGAA	CTATCGTCT	CAAATGTTCA	TCCGCACAGC	TGGTATGTCA	800
AAATGGGGCC	CCTTTTCATA	ATCCTTTCTT	TTTTTCCTT	TCCTCTCTCT	850
ATCTCTCTCT	CTGTTTCTT	TCAACTCGCC	TGATTACAGA	AATTAACCAA	900
CCCCTTGAT	TATAGACGAA	GCCGCCCATC	TCAGCTTCCC	TAGTGGAGCA	950
GATGAAAGCA	AACTCGTTAT	GCCTGGTGAC	AACGTCGAGA	TGATCCTCCA	1000
GACACACCGC	CCCGTGGCTG	CTGAG			1025

## 2) INFORMATION FOR SEQ ID NO: 2200

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Kocuria kristinae*
- (B) STRAIN: ATCC 27570

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200

AGCACGTGCT	GCTCGCCCGC	CAGGTCGGCG	TGCCGACCCCT	GCTGGTCGCC	50
CTGAACAAAGG	CCGACATGGT	CGAGGAGCGAG	GAGCTGCTGG	ACCTCGTCGA	100
GATGGAGGTC	CGCGAGCTGC	TGTCCTCCCA	GGAGTTCGAC	GGCGACAACG	150
CCCCCGTCAT	CCGCGTCTCC	GCGCTGAAGG	CGCTGGAGGG	CGACGAGAAAG	200
TGGGTCAAGT	CCATCGAGGA	GCTCATGGAG	GCCGTGGACG	AGTACATCCC	250
GGACCCCGTG	CGCGACAAGG	ACAAGCCGTT	CCTGATGCC	ATCGAGGACG	300
TCTTCACCAT	CACCGGGCGC	GGCACCGTGG	TGACCGGTG	CGCCGAGCGC	350
GGGACCCCTGG	CCCTGAACTC	CGAGGTCGAG	ATCGTCGGCA	TCCGCCGAT	400
CCAGAACGACC	ACGGTCACCG	GGATCGAGAT	GTCCACAAG	CAGCTCGACG	450
AGGCCTGGGC	CGGCAGAAC	TGCGGTCTGC	TGCTGCGCGG	CCTGAAGCGC	500
GACGACGTCG	AGCGCGGCCA	GGTCGTGGTG	AAGCCGGTT	CCATCACCCC	550
GCACACCAAC	TTCGAGGCAGA	ACGTCTACAT	CCTGTCCAAG	GACGAGGGTG	600
GGCGTCACAA	CCCGTTCTAC	TCGAACTACC	GTCCGCAGTT	CTACTTCCGG	650
ACCACCGACG	TCACCGG				667

## 2) INFORMATION FOR SEQ ID NO: 2201

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Vibrio mimicus*  
 (B) STRAIN: ATCC 33653

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201

TGCTGCAACA	GATGGTCAA	TGCCACAAAC	TCGTGAGCAC	ATCCTGCTGG	50
GTCGCCAAGT	AGGTATTCT	TACATCATCG	TATTCAATGAA	CAAATGTGAC	100
ATGGTTGACG	ATGAAGAGCT	TCTAGAGCTG	GTTGAGATGG	AAGTTCGTGA	150
GCTTCTGTCT	GAGTACGATT	TCCCAGGTGA	TGACCTGCCA	GTAATCCAAG	200
GTTCAAGCACT	AGGCGCGCTA	AACGGCGAAG	CACAGTGGGA	AGCGAAGATT	250
GTTGAAGTAG	CAGAAGCACT	AGATTCAATAC	ATTCCAGAGC	CAGAGCGTGC	300
AGTAGAGACATG	GCATTCCCTGA	TGCCAATCGA	AGACGTATT	TCAATCCAAG	350
GTCGTGGTAC	AGTAGTAACT	GGCCGTATCG	AGCGCGGCAT	CCTGAAAGTG	400
GGTGACGAAG	TTGCGATCGT	TGGTATCAA	GACACAGTAA	AAACTACCTG	450
TACAGGTGTA	GAAATGTCC	GTAAGCTGCT	TGACGAAGGT	CGTGCAGGTG	500
AGAACGTTGG	TGCAGTCTA	CGTGGTACTA	AGCGTGAAGA	AGTAGAGCGT	550
GGTCAAGTAC	TGGCGAAGCC	AGGTTCAATC	ACCCCACACA	CTAAGTTCGA	600
ATCAGAAGTA	TACGTACTGT	CAAAGACGA	AGGTGGCCGT	CATACTCCAT	650
TCTTCAAAGG	TTACCGTCCA	CAGTTCTACT	TCCGTACAAC	TGACGTAACA	700
GGCAGCATCG	AGCTTCCAGA	AGGCGTAGAA	ATGGTAATGC	CAGGCGACAA	750
CATCAAGATG	GTTGTAGACC	TGATTGCA			778

## 2) INFORMATION FOR SEQ ID NO: 2202

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Citrobacter freundii*  
 (B) STRAIN: ATCC 8090

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202

AACGCTGACC	CTGCAGGTAA	TTGCCGCTGC	GCAGCGTGAA	GGTAAAACCT	50
GTGCATTAT	CGATGCAGAA	CACGCACTGG	ACCCGGTCTA	TGCCCCGTAAG	100
CTTGGCGTTG	ATATCGATAA	CCTGCTGTGT	TCTCAGCCGG	ATACCGGTGA	150
ACAAGCGCTG	GAAATCTGTG	ATGCACTGGC	GCGCTCCGGT	GCGGTTGACG	200
TTATCGTTGT	CGACTCCGTT	GCCGCATTGA	CGCCGAAGGC	AGAAATCGAA	250
GGCGAGATTG	GCGACTCTCA	CATGGGCCTT	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCCG	GTAACCTGAA	GCAGTCCAAC	ACGCTGCTGA	350
TTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTTATGTT	CGGTAACCCG	400
GAAACCACCA	CC				412

## 2) INFORMATION FOR SEQ ID NO: 2203

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium botulinum*
- (B) STRAIN: 20:1.2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203

TTTAGATCCA TCTTATGCTA GAAATTTAGG TGTTGATATA GATAACCTAA	50
TAGTTTCTCA ACCAGATACA GGAGAACAGG CTTTAGAGAT AACAGAAGCT	100
TTAGTAAGAT CAGGAGCAGT AGATGTTATA GTTGTAGACT CTGTCAGCAGC	150
TTTAGTTCT AGGGCAGAAA TAGAAGGAGA AATGGGAGAC TCACATGTAG	200
GTCTTCAAGC AAGACTTATG TCTCAAGCCC TAAGAAAATT AGCAGGATCT	250
ATAAATAAAAT CTAAGTGTGT AGCTATATT ATTAAACCAAT TAAGAGAAAA	300
GGTTGGTATA ATGTTTGGAA ATCCAGAAAC AACTCCT	337

2) INFORMATION FOR SEQ ID NO: 2204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Francisella tularensis*
- (B) STRAIN: ATCC 29684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204

AAAGCAAGGC GGTACTGCAG CATTGTTGA TGCTGAGCAT GCACTAGATC	50
CAAAATATGC AAAGCTTTA GGTGTTGATG TTGATAATCT GATCGTGTCA	100
CAGCCGGATA CGGGTGAGCA AGCTTTAGAG ATTGCTGATA TGTTGGTACG	150
TTCTGGAGGA GTTGATATTG TAGTAATTGA CTCTGTTGCT GCACTTACGC	200
CAAAGGCAGA GATTGAGGGT GACATGGCG ACTCGCACAT GGGCTTACAA	250
GCAAGATTAA TGTCACAAGC ACTAAGAAAA CTAACGGCAA ATATCAAGCG	300
CTCAAATACT CTAGTGATAT TCATTAACCA AATTCTGTATG AAGATCGGGG	350
TTATGTTGG TAACCCTGAA ACTACAAC	379

2) INFORMATION FOR SEQ ID NO: 2205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus anaerobius*
- (B) STRAIN: ATCC 27337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205

ACTTGACCCA	GTATATGCAA	GGGCTCTTGG	AGTGGATATA	GACAACCTAG-	50
TCATATCTCA	GCCAGATACA	GGAGAACAGG	CCCTAGATAT	AGCAGAGTCC-	100
CTTATAAGAT	CAGGAGCTGT	AGATATACTA	GTAATAGACT	CAGTAGCTGC-	150
CCTAGTACCT	AAGGCAGAAA	TAGAAGGTGA	CATGGGAGAT	TCTCACGTAG-	200
GTCTACAGGC	TAGACTTATG	TCACAGGCAC	TTAGAAAATT	GACTGGATCT-	250
ATAAAGAAGT	CAAACGTGT	TGTTATATT	ATCAACCAGT	TGAGAGAAAA-	300
AGTAGGGGTT	ATGTTCGGTA	ATCCAGAGAC	AACAACA		337

2) INFORMATION FOR SEQ ID NO: 2206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Peptostreptococcus asaccharolyticus*
- (B) STRAIN: LSPQ 2639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206

TCTTGATGCT	GGATATGCAA	AAAACCTTGG	AGTAGATGTA	GAAAATTAA-	50
TTATTTCTCA	ACCTGATACA	GGTGAGCAAG	CCCTAGAAAT	AACTGAAGCT-	100
CTTGTAAGAT	CTAACGCTGT	TGATTAAATT	ATTATAGACT	CAGTTGCCGC-	150
ACTTGTACCA	AAAGCAGAAA	TCGATGGTGA	CATGGGAGCT	GCACAAATAG-	200
GTCTTCAAGC	AAGACTTATG	TCTCAAGCTC	TTAGAAAATT	AACTGGGGCA-	250
ATCAACAAGT	CAAAATGTAC	CGTTGTATT	ATTAACCAAC	TTAGAGAAAA-	300
AGTTGGTATC	ATGTTGGTA	ACCCAGAAAC	TACAACA		337

2) INFORMATION FOR SEQ ID NO: 2207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Providencia stuartii*

(B) STRAIN: ATCC 33672

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207

CTCACGTTGC	AAGTTATTGC	AGCAGCACAA	CGTAGCGGAA	AAACCTGTGC	50
ATTTATCGAC	GCTGAACATG	CGCTAGATCC	AATCTATGCG	AAAAAAACTGG	100
GTGTTGATAT	CGATAACCTT	CTATGTTCTC	AACCTGATAC	TGGTGAGCAA	150
GCATTAGAGA	TTTGTGATGC	ACTGACGCGT	TCAGGCGCTG	TTGATGTCAT	200
TATCGTTGAC	TCCGTGGCCG	CATTAACACC	AAAAGCTGAA	ATTGAAGGTG	250
AAATCGGTGA	CTCACACATG	GGCTTAGCGG	CTCGTATGAT	GAGCCAAGCG	300
ATGCGTAAAT	TAGCGGGTAA	CTTAAAGAAC	TCGAATACAC	TTTTAATCTT	350
CATTAACCAA	ATCCGTATGA	AGATTGGCGT	TATGTTGGT	AACCCAGAAA	400
CCACTACA					408

2) INFORMATION FOR SEQ ID NO: 2208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis* serotype Paratyphi A
- (B) STRAIN: ATCC 9150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208

GCTGCAGGTG	ATTGCCGCTG	CGCAGCGTGA	AGGTAAAACC	TGTGCGTTA	50
TCGATGCGGA	ACACGCGCTT	GACCCTGTTT	ACGCACGCAA	GCTGGGCGTC	100
GATATCGATA	ACCTGCTTTG	TTCTCAGCCG	GATACCGGCG	AGCAGGCGCT	150
GGAAATCTGT	GACGCGCTGG	CGCGTTCAAG	CGCGGTGGAC	GTCATTGTGG	200
TCGACTCCGT	AGCGGCGCTA	ACGCCGAAAG	CGGAAATCGA	AGGCGAAATT	250
GGCGACTCTC	ACATGGGCCT	CGCGGCGCGT	ATGATGAGCC	AGGCGATGCG	300
TAAGCTGGCG	GGGAACCTAA	AACAGTCCAA	CACGCTGTTG	ATTTTCATCA	350
ACCAGATCCG	TATGAAGATT	GGCGTGATGT	TCGGTAACCC	GGAAACCACC	400
ACC					403

2) INFORMATION FOR SEQ ID NO: 2209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Salmonella choleraesuis* subsp. *choleraesuis*  
 serotype Typhimurium  
 (B) STRAIN: ATCC 14028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209

GACCCTGACG	CTGCAGGTGA	TTGCCGCTGC	GCAGCGTGA	GGTAAAACCT	50
GTGCGTTTAT	CGATGCGGAA	CACGCGCTTG	ACCCTGTTA	CGCACGCAAG	100
CTGGCGCTCG	ATATCGATAA	CCTGCTCTGC	TCTCAGCCGG	ATACCGGCGA	150
GCAGGCCTG	GAAATCTGTG	ACCGCGCTGGC	GCGTTCAGGC	GCGGTGGACG	200
TCATTGTTGGT	CGACTCCGTA	GCGGCGCTAA	CGCCGAAAGC	GGAAATCGAA	250
GGCGAAATCG	GCGACTCTCA	CATGGGCCTC	GCGGCGCGTA	TGATGAGCCA	300
GGCGATGCGT	AAGCTGGCGG	GGAACCTGAA	ACAGTCCAAC	ACGCTGTTGA	350
TTTCATCAA	CCAGATCCGT	ATGAAGATTG	GCGTGATGTT	CGGTAAACCCG	400
GAAACCACCA	CC				412

2) INFORMATION FOR SEQ ID NO: 2210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus saprophyticus*
- (B) STRAIN: ATCC 15305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210

ATTAGATCCT	GTTTACGCCAG	AAGCTTTAGG	CGTAGATATA	CAAAATTTAT-	50
ATTTATCTCA	ACCTGATCAT	GGGAAACAAG	GTTTAGAAAT	TGCCGAAGCA-	100
TTTGTAGAA	GTGGCGCTGT	TGATATCGTT	GTGGTCGATT	CAGTTGCTGC-	150
GCTTACACCT	AAAGCTGAAA	TTGAAGGTGA	AATGGGAGAT	ACGCACGTTG-	200
GTTTGCAAGC	ACGTCTTATG	TCCAAGCCT	TGAGAAAGCT	TTCCGGTGCA-	250
ATTTCAAAAT	CAAATACAAC	AGCAGTATTT	ATCAACCAAA	TCCGTGAAA-	300
AGTTGGTGTG	ATGTTCGGTA	ATCCTGAAGT	TACACCA		337

2) INFORMATION FOR SEQ ID NO: 2211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211

GACACTGACA	TTACAGGTTA	TCGCCGCCGC	ACAGCGTCAA	GGCAAAACGT	50
GTGCATTAT	CGATGCCGAA	CATGCCCTTG	ACCCAATCTA	TGCCAAGAAA	100
TTGGGTGTAG	ATATTGATAA	CCTACTGTGT	TCTCAGCCAG	ATACTGGCGA	150
GCAGGCACTG	GAAATTGTG	ATGCGCTGAC	TCGCTCTGGT	GCGGTTGACG	200
TTATCATCGT	TGACTCCGTA	GCGGCATTGA	CACCAAAAGC	TGAAATTGAA	250
GGTGAATTG	GCGATTCTCA	TATGGGCCTT	GCCGCGCGTA	TGATGAGCCA	300
GGCTATGCGT	AAGCTGGCGG	GTAACCTGAA	GAATGCGAAT	ACCTTACTGA	350
TTTTATCAA	CCAAATCCGC	ATGAAAATTG	GCGTATGTT	TGGTAACCCA	400
GAAACCACTA	CC				412

## 2) INFORMATION FOR SEQ ID NO: 2212

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212

CACGCTCACC	TTGCAAACCA	TCGCCGAAAT	GCAAAACTG	GGCGGCACCT	50
GCGCGTTAT	CGACGCCGAG	CACGCACTGG	ACGTCACGTA	CGCGCAAAAG	100
CTGGGCGTCA	ACCTGAGCGA	TCTGCTGATC	TCGCAACCGG	ACACCGGCGA	150
ACAAGCGCTG	GAAATCTGCG	ACGCCCTGGT	GCGTTCCGGT	TCGGTGGACA	200
TGGTCGTGAT	CGACTCGGTC	GCCGCGCTGA	CCCCGCGCGC	CGAGATCGAA	250
GGCGACATGG	GCGATTGCT	GCCAGGTTTG	CAGGCACGTT	TGATGTCGCA	300
AGCACTGCGC	AAGCTTACCG	GTTCGATCAA	CCGCACCAAAC	ACCCTGGTCA	350
TCTTCATCAA	CCAGATCCGC	ATGAAAATCG	GCGTCATGTT	CGGCAGCCCG	400
GAAA					404

## 2) INFORMATION FOR SEQ ID NO: 2213

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213

CGTGCCATTG ACATGATTTC CGAAGAAGAC GCTGAAGGCA CG

## 2) INFORMATION FOR SEQ ID NO: 2214

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214

CAACTACATT ACGTTCTGCA ACACAAGGTC GTGGTACTTT CAGTATGACA	50
TTTGACCACT ATGAAGATGT TCCTAAGAGC ATTGCAGAAG AAATCATCAA	100
GAAAAATGGC GGTAACGGAG AATAA	125

## 2) INFORMATION FOR SEQ ID NO: 2215

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215

CGACTCAAAT GCGTTCTATG TCTCAAGGTC GTGCGACATA CTCAATGGAA	50
TTTGCTAAAT ATGCTGAAAC TCCACGTAAC GTGGCTGAAG GCATCATCGC	100
TAAATTCCAA GCTGGCGGTA AAAAAGGTGA CGACGAGTAA	140

## 2) INFORMATION FOR SEQ ID NO: 2216

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Actinomyces meyeri*  
 (B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216

CCGGTGACCT GCGTTCTAAG ACGCAGGGTC GCGCTGTCTA CTCCATGGAG	50
TTCGACAGCT ACGCCGAGGT TCCGCGCGCG GTCGCGGATG AGATCGTCGG	100
CAAGTCTCGG GGCAACTGA	119

## 2) INFORMATION FOR SEQ ID NO: 2217

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Clostridium difficile*  
 (B) STRAIN: ATCC 9689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217

CGACCGACGT TCGCTCCATG TCCCAGGGTC GCGCAAGCTA CTCTATGGAA	50
TTCAAAAAAT ACAACACAGC TCCGGCGCAC ATCGCTGAAA CTGTATCCAA	100
AAAACAAGGC TGA	113

## 2) INFORMATION FOR SEQ ID NO: 2218

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Corynebacterium diphtheriae*  
 (B) STRAIN: ATCC 27010

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218

GCGACCTGCG TTCCCGTACC CAGGGCCGTG CAAACTACAC CATGATCTTC	50
GACTCCTACG CTGAGGTTCC TACCAACGTG GCAGCTGAGA TCGTGGCAGA	100
GCGCAACGGC ACTGCCTAA	119

## 2) INFORMATION FOR SEQ ID NO: 2219

1140

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCTAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AGTAA	115

2) INFORMATION FOR SEQ ID NO: 2220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220

AACTCAGCTG CGTTCTCTGA CCAAAGGTCG TGCATCATAC ACCATGGAAT	50
TCCTGAAGTA TGATGATGCG CCGAACAAACG TTGCTCAGGC CGTTATTGAA	100
GCCCGTGGTA AATAA	115

2) INFORMATION FOR SEQ ID NO: 2221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221

CAACTCACCT TCGTTCAGGT ACGCAAGGTC GTGGTGTATA CACTATGCAA	50
TTTGACCACT ATGAAGAAGT TCCTAAATCT ATTGCTGAAG AAATCATTAA	100
AGCTAATGGT GGA	113

2) INFORMATION FOR SEQ ID NO: 2222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222

CGGCGACCTG CGGTCCAAGA CCCAAGGCCG GGCAGACTAC TCCATGGTCT	50
TCGACTCCTA CGCCGAAGTG CCGGCCAACG TGTCGAAGGA GATCATCGCG	100
AAGGCGACGG GTCACTGA	118

2) INFORMATION FOR SEQ ID NO: 2223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordonaee*
- (B) STRAIN: Mgord-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223

CCGGCGACCT GCGGTCCAAG ACGCAAGGCC GGGCGAACTA CTCCATGGTG	50
TTCGACTCGT ACGCCGAAGT TCCGGCGAAC GTGTCGAAGG AGATCATCGC	100
GAAGGCGACG GGCGAATAG	119

2) INFORMATION FOR SEQ ID NO: 2224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasi*
- (B) STRAIN: Mkan-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224

CGGCGACCTG CGGTCCAAGA CTCAAAGGCCG GGCGAACTAC TCGATGGTGT	50
TCGATTCTA CGCCGAAGTG CCGGCTCAGG TGTGAAAGGA GATCATCGCG	100
AAGGCGACTG GCGAGTGA	118

2) INFORMATION FOR SEQ ID NO: 2225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225

CGGAGACTTG CGGTGAAAGA CCCAGGGCCG GGCGAACTAC TCCATGGTGT	50
TCGACTCCTA CGCCGAAGTG CCGGCGCAGG TGGCGAAGGA GATTATCGCG	100
AAGGCAACGG GCGAGTAA	118

2) INFORMATION FOR SEQ ID NO: 2226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226

GACCGACCTG CGTTCTGCAA CCCAAGGCCG CGCTACTTAC TCTATGGAGT	50
TCAAGAAATA TTCTGAAGCT CCTGCCACA TAGCTGCTGC TGAACTGAA	100
GCCCGTAAAG GCTAA	115

## 2) INFORMATION FOR SEQ ID NO: 2227

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 118 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Staphylococcus epidermidis*
  - (B) STRAIN: ATCC 14990
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227

AACTTCATTA CGTTCTAACCA CGCAAGGTCG CGGTACTTAC ACAATGTACT	50
TTGACCACTA TGCAGAAGTT CCTAAATCAA TTGCTGAAGA AATCATCAAG	100
AAAAATAAAG GTGAATAA	118

## 2) INFORMATION FOR SEQ ID NO: 2228

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 118 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Staphylococcus haemolyticus*
  - (B) STRAIN: ATCC 29970
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228

AACTTCATTA CGTTCTAACCA CTCAAGGTCG CGGTACTTAC ACTATGTACT	50
TCGATCACTA TGCAGAAGTT CCAAAATCAA TTGCTGATGA TATCATCAA	100
AAAAATAAAG GTGAATAA	118

## 2) INFORMATION FOR SEQ ID NO: 2229

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1630 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Succinivibrio dextrinosolvens*  
 (B) STRAIN: ATCC 19716

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229

CGTTCAATGC	GTGTTCTAGA	CGGTGCAGTT	ATGGTTTACT	GTGCTGTGGG	50
TGGTGTTCAG	CCTCAGTCTG	AAACC GTT T G	GAGACAGGCT	CAGAAGTACA	100
AGGTTCCCTCG	TATTGCTTTC	GTAAATAAGA	TGGACCGTAC	TGGTGCTAAT	150
TTCCTACGTG	TTGTAGAGCA	GATTAAGACC	CGTCTAAAGG	GTAAACCTGT	200
TCCTCTAATG	TTACCTATCG	GTAAAGAGGA	CAGCTTTGTT	GGTGTAGTTG	250
ACCTAATCAA	GCGTAAGGCT	ATCGACTGGG	ATGAGGCATC	TCAGGGTATG	300
AAGTTTGAGT	ACGTTGACAT	TCCAGCAGAT	ATGGTTGAGG	AAGTTGAAGA	350
GTGGCGTGCA	AAGCTTGAG	AAGCAGCTGC	AGAAGCTAAC	GACCGAGCTGA	400
TGGATAAATT	CTTCGGTGGT	GAAGAGCTGA	CCGAGGAAGA	GATCAAGGCT	450
GCTCTACGTG	AGCGTACTCT	TCGCAACGAA	ATTATTCTA	TGTGCTGC GG	500
TTCAGCATT	AAGAACAAAGG	GTGTTCAGGC	AATGCTTGAC	GCTGTTGTTG	550
AGTATCTTCC	ATCTCCAGCA	GATGTTCC TG	CTGTTGAGGG	TAAGACCTA	600
ACCGGTGAAG	CTGATACTCG	TAAGGCTGAC	GATAAAAGAC	CATTCTCTGC	650
TTTAGCATT	AAGCTAGCAA	ATGACCCATT	CGTAGGTAAC	TTAACATTCT	700
TACGTTGCTA	CTCAGGCTTT	ATTAAGTCTG	GTGACACTGT	AATGAAC TCA	750
GATAAGCAGA	AGCGTGAGCG	TTTCGGCCGT	CTAGTTCAGA	TGCACGCTAA	800
TGCTCGTAAT	GAGGTTAGCG	AGGTTTATGC	AGGTGACATC	GTTGCTGCTA	850
TTGGTCTGAA	GGAAACCGTT	ACCGGTGATA	CCTTATGTGA	CCCAGAGCAT	900
CCAATCATT	TTGAGTCAAT	CGACTTTGCA	GAGCCAGTTA	TCTCTGTAGC	950
AGTTGAGCCT	AAGACCAAGG	ACGATCAGGA	GAAGATGGCT	CTTGCTTTAC	1000
AGCGTTTAGC	AAAAGAAGAT	CCTTCATTCC	GC GTT CGTAC	AGACGAAGAG	1050
TCTGGCCAGA	CCATTATTTC	TGGTATGGT	GAGCTTCACC	TAGACATCAT	1100
TGTTGACCGT	CTACGCCGTG	AGTTCAAGGT	TGAGTGTAAT	CAGGGTAAGC	1150
CACAGGTTGC	ATACCGTGAG	ACCATTAAGA	GCAAGGTTGA	ACAGCAAGGT	1200
AAGTTTGCTC	GTCAGTCTGG	TGGTCGTGGT	CAGTACGGTG	ACTGCTGGTT	1250
ACGTATGGAA	CCTCTTGAGC	CAGGTAAAGGG	CTACGAATTC	GTGAATGAGA	1300
TTGTTGGTGG	TGTAATTCT	AAGGAATATA	TCCCTGCAAT	TGATAAGGGC	1350
TGTCAGGAGC	AGATCGCTAA	CGGTGTTCTA	GCTGGTTTCC	CAGTTGTTGA	1400
CATCAAGATC	ACTGTATTCTG	ATGGTTCTTA	CCACGAAGTT	GA CTT CAG	1450
AAATGGCATT	CAAGATTGCT	GCTTCTATGG	CATTCAAAGA	GGGCTTCAAG	1500
AAGGCAAATC	CTGTTCTTCT	AGAGCCTTTA	ATGAAGGTAG	AAGTTGATAC	1550
TCCTGAAGAC	TACATGGGTG	ACGTTATTGG	TGACTTAAAC	CGTCGTCGTG	1600
CTATCGTTGA	AGGCATGGAA	GATGGTCCTA			1630

## 2) INFORMATION FOR SEQ ID NO: 2230

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1662 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tetragenococcus halophilus*  
 (B) STRAIN: ATCC 33315

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230

TTGAAGTGCA	ACGTTCAT	TG	CGTGTGCTAG	ACGGTTCA	GT	TACTGTCTTG	50		
GA	CTCACAA	AT	CAGGTGTTGA	ACCACAA	ACT	GAAACAGTT	100		
AACAGA	ATAT	CAAGTAC	CTC	GTATTGTATT	CTGTAATAA	ATGGATAA	150		
TTGGCG	CAGA	TTTCTTAT	AT	TCTGTCCGAT	CATTGCATGA	TCGTTAGAA	200		
GCTAATGC	AC	ACCTATCCA	ATTGCCA	ATT	GGTGTGAAG	ATAACTTGA	250		
AGGTATCATC	GAC	CTTGTA	AGATGAA	AGC	TGAATT	AAAGATGATT	300		
TAGGGACTAC	TTTCGA	AGAA	ACTGAA	ATCC	CAGATGAATA	TAAAGAAACA	350		
GCTCAAGA	AT	GGCATAATAA	TTTGGTAGAA	TCTGTAGCTG	ATT	TTGATGA	400		
AGATATCATG	ATG	GAAGGTGA	AGAA	ATTACA	CCTGAA	GAGT	450		
TACAAGCAGG	TAT	TCTGTA	AA	CAACATTAT	CTGTTGA	ATT	ACCCAGTA	500	
TTATGTGGTT	CTG	CATTAA	AA	ACAAAGGT	GTCAAATGA	TGTTGGATGC	550		
AGTAATTGAT	TACT	TGCTT	CTCC	AAACCCGA	CGT	TTGAGGGA	600		
TCGATCCGAA	AA	ACAGATGAA	GAA	ACTGAA	ATCCTGCTG	TGATAGTGAG	650		
CCTTTTCAT	CA	CTTGCTT	TAA	AGTTATG	TCAGAC	CCCT	ATGTTGCCG	700	
CTTAAC	TTTC	TTCCGTGTT	AT	CAGGTGT	GTTG	GATACA	GGTTCTTATG	750	
TATTGAATGC	TACT	AAGGGT	TCAC	GTGAAC	GAATTGGTC	TAT	TTGCAA	800	
ATGCATGCCA	ATT	CTCGTT	TGAG	ATCGAT	AAGGTT	TATT	CAGGTGACAT	850	
TGCAGCTGCT	GTAGG	GCTGA	AGAAC	ACTAC	AACAGGG	ATC	CTTGTG	900	
ATGAGAAAAA	TCCAG	TTATT	TTGG	AAACTA	TCAACT	TCCC	TGAACCAGTA	950	
ATTCAAGTTG	CTG	TGAACC	TAAG	TCAAA	GCTGAC	CAAG	ATAAAATGAG	1000	
CGTAGCACTA	CAAAA	ACTTG	CAGA	AGAAGA	CCC	ATCTTT	AAAGTGGAAA	1050	
CCAACGCTGA	AACT	GGCGAA	ACTG	TAATTG	CTGGT	ATGGG	TGAAC	TTCAA	1100
TTAGACGTT	TC	TATTGACCG	TATG	AAAGACT	GAATT	TTAAAG	TGGATGCCA	1150	
TATTGGTGCA	CCAC	AAAGTT	CTTAT	CGTGA	AACT	TTCCGT	TCATCA	ACTA	1200
AAGCTGAAGG	GAA	ATT	TATC	CGCC	AA	CTG	TGTTAGAGG	TCAATACGGT	1250
CACGTATGGG	TTG	AATT	TAC	TCCAA	ACG	GAAGGAGCAG	GATT	CGAATT	1300
AAAAAACTCC	ATT	GTTGGTG	GGG	TTGTCCC	TCG	TGACTAT	ATAC	CTGCAG	1350
TACAAAAAAGG	ACT	GGAA	AGAC	GCC	ATGG	GTGTT	AGCT	GGTTAT	1400
CCATTAGTTG	ACG	TAAAGGC	AGA	ACTGTT	GAT	GGTTCTT	ACC	ATGACGT	1450
CGACTCTAAT	GAA	ACAGCCT	TCC	GTATTG	GG	CTTCAATG	TCT	CTACGTG	1500
AAGCTGCGAA	AA	AGGCA	GAT	CCAGT	TT	GAA	GATGAA	AGTA	1550
ACAATTAGTA	TCC	CTGAAGA	AT	ATCTAGGT	GAT	ATTATGG	GACAT	GTTTAC	1600
AGCTCGTCGT	GGT	CGTGT	TTG	AAGGA	TG	CTCACGGT	AAT	GCACAAA	1650
CTGTAATGC	GT								1662

## 2) INFORMATION FOR SEQ ID NO: 2231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Veillonella parvula*
- (B) STRAIN: ATCC 10790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2231

AAGTAGAACG	TTCTCTACGT	GTACTTGACG	GTTCTGTTGC	GGTGTTCAGT	50
GCTAAAGGTG	GCGTTGAACC	TCAATCCGAA	ACAGTATGGC	GTCAGGCTTC	100
TAAC	ACTACGGC	GTACCTCGTA	TCGCTTATGT	AAATAAGATG	150

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GTGCTGACTT	CTTCAACGTA	GTTGACATGA	TGAAAGCTCG	TTTGGGTGCA	200
AATTCCGTAG	CTATCCAAGT	ACCAATCGGT	GCTGAAGATA	CTTCGAAGG	250
CATCATTGAC	TTGATGACTA	TGAAAGCGGA	AATTATATAA	TCCGATGACG	300
GTAAAGAATA	TGAAATCACT	GATATCCCTG	CTGAATATCA	AGAAGTAGCA	350
GAAGCTCGTC	GCGAAATGAT	GATCGATGCT	ATCGCTGAA	CAGATGATGA	400
TATCATGATG	AAATATTGG	AAGGCGAAGA	AATTCTGTG	GAAGAATTGA	450
AAGCGGCATT	GCGTAAAGCT	GTTATTGCTA	ACCAATTATT	CCCAGTTCTT	500
TGTGGTTCTT	CCTATAAAA	TAAAGGTGTT	CAAATGTTAT	TGGATGCTGT	550
TATCGATTAC	ATGCCAGCTC	CAATCGACAT	CCCACCTATT	AAAGGTGTTG	600
TTCCTGGTAC	TGAAGAAGAA	ACAACTCGTC	CTTCTTCCGA	TGAAGAGCCA	650
TTCTCTGCAT	TGGCATTCAA	AATCATGGCT	GACCCCTATG	TTGGTAAATT	700
AGCGTTCTTC	CGTGTGTACT	CCGGTACATT	GGAATCTGGC	TCCTACGTTT	750
TCAACTCCAC	TAAAGGTAAA	AAAGAACGTA	TCGGTCGTAT	TCTTCAAATG	800
CACGCTAACT	CCCGTAAAGA	AATCGAACGC	GTATATTCTG	GTGACATCGC	850
TGCGGCCGTT	GGCTTAAAGG	ATACTACTAC	AGGGACACAA	TTGTGTGATG	900
AAAAATCTCC	TGTAATCCTT	GAGTCCATGG	AATTCCCTGA	ACCAGTTATC	950
TCCGTTGCTG	TTGAACCTAA	ACACAAAGCT	GACCAAGAAA	AAATGGGTAC	1000
AGCTCTTGCT	CGTTTGGCAG	AAGAAGATCC	TACTTTCAA	GTTCGTACTG	1050
ATGAAGAAC	AGGTCAAAC	ATTATCTCTG	GTATGGCGA	ACTTCACTTG	1100
GATATCATCG	TTGACCGTAT	GAACCGTGAA	TTCAAAGTAG	ATTGTAACGT	1150
AGGTAAACCT	CAAGTAGCAT	ACCGCGAAC	TATCCGTA	GCTGTTAAGG	1200
CTGAAGGTAA	ATTCGTACGT	CAATCTGGTG	GTCGTGGTCA	ATATGGTCAC	1250
TGCTGGTTGG	AATTGATTCC	TCAAGAACCA	GGTGTGGCT	TCGAGTTTG	1300
AAACAAGGTT	GTAGGTGGTG	CGATTCCCTG	TGAATACATC	GGACCTGTTG	1350
AAAGCGGTGT	TAAAGAAGCT	ATGGAATCCG	GTGTTATCGC	TGGGTACCC	1400
ATGGTTGATG	TTAAAGTTAT	CGTATTGAT	GGTTCTTACC	ATGACGTTGA	1450
CTCCAACGAA	ATGGCCTTCA	AAATTGCTGG	TTCTATGGGC	TTCAAAGAAG	1500
GTGCTCGCAA	AGCAGACCC	GCATTGCTTG	AACCATA	GGCTGTAGAA	1550
GTAGACGTT	CTGAAGAATA	CATGGGCGAC	GTTATCGGTG	ACTTGAAC	1600
TCGTCGTGGT	CGCATGGACG	GCATGGAAGC	TCGTAATGGT	TCCCAACATA	1650
TC					1652

## 2) INFORMATION FOR SEQ ID NO: 2232

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1624 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Yersinia pseudotuberculosis*
- (B) STRAIN: ATCC 29833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232

AGTAGAGCGT	TCCATGCGTG	TTCTTGACGG	CGCGGTAATG	GTAACTGTG	50
CAGTTGGTGG	TGTTCAGCCA	CAGTCTGAAA	CCGTATGGCG	TCAGGCTAAT	100
AAATATAAAG	TTCCACGTAT	TGCGTTCGTT	AAACAAATGG	ACCGTATGGG	150
TGCGAACTTC	CTGCGCGTAG	TTGGTCAACT	GAAATCTCGC	CTTGGTGCAG	200
ACCCAGTTCC	ACTGCAGTTG	GCAATTGGCG	CAGAAGAAAA	ATTCAACCGGT	250
ATTATCGATC	TGGTAAAAT	GAAAGCGATC	AACTGGAACG	AAGCTGATCA	300
GGCGGTGACC	TTCGAATATG	AAGAAATCCC	TGCTGATATG	GCTGAACCTGG	350

CTGCTGAATG	GCACCAGAAT	CTGGTTGAAT	CTGCGGCAGA	AGCGTCTGAC	400
GAGCTGATGG	ACAAATACTT	GGGTGGCGAA	GAGCTGACCG	AAGAAGAAAT	450
CAAGAAAGCT	TTACGTCAAC	GTGTTCTGAA	AAGCGAAATT	ATTCTTGTAA	500
CCTGTGGTTC	TGCCTTAA	AACAAAGGCG	TACAGGCAAT	GCTGGATGCG	550
GTTATTGAGT	ACCTGCCTGC	ACCAACTGAC	GTTGAATCAA	TCAACGGCAT	600
CTTGGATGAT	GGCAAAGATA	CTCCGGCTGT	TCGTCAATTCT	GACGACAAAG	650
AGCCGTTCTC	TGCTCTGGCG	TTCAAAATCG	CTACCGACCC	ATTCTGGGT	700
AACCTGACGT	TCTTCCGCGT	GTACTCTGGT	ATTGTTAATT	CCGGTGATAC	750
CGTTCTGAAC	TCAGTGAAT	CGCAACGTGA	ACGCTTAGGT	CGTATCGTAC	800
AGATGCACGC	TAACAAGCGT	GAAGAGATCA	AAGAAGTTCA	CGCCGGTGAT	850
ATCGCAGCCG	CTATCGGTCT	GAAAGATGTG	ACTACGGGTG	ACACTTTGTG	900
TGACCCGAAT	AATCCGATCA	TCTTGGAACG	TATGGAGTTC	CCAGAGCCGG	950
TAATCTCTGT	TGCTGTTGAA	CCAAAAACCA	AAGCTGACCA	AGAAAAAAATG	1000
GGTATGGCTC	TGGGGCGTTT	GGCGAAAGAA	GATCCATCAT	TCCCGTGGTTG	1050
GAATGACGAA	GAATCTGGTC	AGACTATCAT	CGCTGGTATG	GGTGAGTTGC	1100
ATTGGATAT	CCTGGTTGAC	CGTATGCGCC	GCGAATTAA	CGTGGAAAGCA	1150
AACGTCGGTA	AACCTCAGGT	TGCGTACCGT	GAAACTATCC	GCGAAACCGT	1200
TAAGGATGTG	GAAGGTAAGC	ACGCTAAGCA	GTCAGGCGGT	CGTGGTCAGT	1250
ATGGTCATGT	TGTTATCGAC	ATGTCTCCAT	TGCCACCGGG	TGGTGTGTTGGG	1300
TATGAATTG	TCAACGAAAT	CGTTGGTGGT	TCTATTCCCA	AAGAATTTCAT	1350
TCCGGCCGTT	GATAAAAGGTA	TTCAAGAAC	GCTGAAATCT	GGCCCTCTGG	1400
CAGGTTACCC	AGTTGTTGAC	GTAAAGTGC	GTCTGCACTA	CGGTTCTTAC	1450
CATGACGTTG	ACTCCTCAGA	ATTGGCATT	AAATTAGCTG	GTTCTATCGC	1500
CTTTAAAGAA	GGTTTCAAC	GAGCTAAACC	AGTTCTGCTT	GAGCCAATCA	1550
TGAAGGTTGA	AGTCGAAACC	CCTGAAGATT	ACATGGGTGA	CGTAATGGGC	1600
GACCTGAACC	GTCGTCGCGG	TATC			1624

## 2) INFORMATION FOR SEQ ID NO: 2233

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1636 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Zoogloea ramigera*
- (B) STRAIN: ATCC 25935

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233

GAACGCTCGA	TGCGCGTGCT	TGACGGTGCT	TGCATGGTTT	ACTGCGCAGT	50
GGGCGGTGTT	CAGCCACAGT	CGGAAACCGT	GTGGCGTCAG	GCTAACAAAGT	100
ACAAAGTGCC	ACGTCTGGCC	TTCGTCAACA	AGATGGACCG	TACCGGGGCC	150
AACTTCTTCA	AGGTGTACGA	GCAGATGCGT	GCTCGCCTGA	AGGCCAACCC	200
GGTCCTGATC	CAGATCCCTA	TCGGCGCTGA	AGACAACCTC	AAAGGCGTGA	250
TCGATCTGGT	CAAGATGAAG	GCTATCCTGT	GGGACGAAGC	GTCGCAAGGC	300
ATGAAATTG	ACTACGTCGA	TATTCTGCA	GAGCTGGCTG	ATTGGGCCGC	350
CGAGTGGCGC	AAAAAGATGG	TTGAAGCTGC	TGCTGAAGCC	ACCGAAGAGC	400
TGATGAACAA	GTACCTGGAA	GAAGGCAGAC	TGACCGAAGC	CGAGATCAAG	450
CAGGCGCTGC	GTACCCGTAC	CATCGCTTCG	GAAATCGTTC	CGATGATGTG	500
CGGTACCGCC	TTCAAGAAC	AGGGCGTACA	GGCCATGCTG	GACGCGGTCA	550
TCGAATACCT	GCCATCGCCA	CTGGACATCG	ACGATGTCGG	CGGTACGGAC	600

GAAGACGACC	AGCCAACCAC	CCGTCGCGCA	GCTGACGACG	AGAAATTCTC	650
GGCGCTGGCC	TTCAAGATCA	TGACCGACCC	GTTCGTCGGT	CAATTGGCCT	700
TCTTCCCGGT	GTACTCGGGC	GCCGTCAATT	CGGGCGACAC	CGTGTACAAC	750
TCGGTCAAAG	GTCGTAAAGA	GGCTCTGGGC	CGTATTCTGC	AGATGCACGC	800
GAATCAGCGC	GAAGAGATCA	AAGAAGTGC	CGCCGGCGAC	ATCGCCGCTG	850
CGGTTGGCCT	GAAAGACGTG	ACACGGGGC	AAACACCTGTG	CGATCCGACC	900
GCCATCATCA	CGCTGGAAAA	AATGATCTTC	CCTGAGCCTG	TGATTCAACA	950
GGCAGTCGAG	CCAAAAAACCA	AGGCCGACCA	GGAAAAAAATG	GGCCTGGCAC	1000
TGAACCGCCT	GGCACAGGAA	GATCCTTCGT	TCCCGGTGAA	GACCGATGAA	1050
GAATCGGGCC	AGACCATCAT	CGGTGGWATG	GGCGAGCTGC	ACCTGGAAAT	1100
TATCGTTGAC	CGCATGAAGC	GCGAATTCCG	CGTGGAAAGCA	ACCGTCGGCA	1150
AGCCACAAGT	GGCTTACCGC	GAAACGATCC	GTAAAACCTG	CGAAGAAATCG	1200
GAAGGCAAGT	TCGTCAAGCA	ATCCGGTGGT	CGTGGTCAAT	ACGGTCACGT	1250
TGTGCTGAAG	ATCGAGCCGC	AAGAACCAAGG	CAAGGGCTTC	GAGTTCGTTG	1300
ACGCCATCAA	GGGCGGTACC	GTTCTCGCG	AGTACATCCC	TGCGGTGGAA	1350
AAAGGCGTGC	GCGGCACCC	GAACACCGGC	GTGCTGGCTG	GTTACCCGGT	1400
CGTGGACGTC	AAGGTACCGC	TGTTCTTCGG	TTCGTACAC	GATGTGGACT	1450
CGAACGAAAA	CGCGTTCCAG	ATGGCCGCTT	CGATGGCATT	CAAAGAAGGC	1500
TGCCGCAAAG	CATGCCAGT	CATTCTGGAG	CCAATGATGG	CTGTGGAAGT	1550
GGAAACGCCG	GAAGACTACG	CCGGTACCGT	GATGGGCGAC	CTGTCGTCCC	1600
GCCGCGGTAT	GGTGCAGGGC	ATGGACGAAA	TCCCAG		1636

## 2) INFORMATION FOR SEQ ID NO: 2234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234

GGCACGAACG	ATCTTGGCCGG	ACGGGCCATC	TTCCATACCT	TCGATCAGGC	50
CACGACGACG	GTTCAGGTCA	CCGATCACGT	CGCCCCATATA	GTCTTCCGGT	100
GTCTCGACTT	CTACTTTCAT	GATCGGTTCG	AGCAGAACCG	GGTTGGCCTT	150
CATGAAGCCA	GCCTTAAAGG	CCATGGAAGC	AGCGATCTTG	AACGCCAGTT	200
CGGAAGAGTC	GACATCGTGG	TAGGAACCGA	AGTGCAGACG	CACGCCAGA	250
TCCATAACCG	GATAACCTGC	CAGCGGGCCG	GACTTCAGTT	GCTCGCGGAT	300
ACCCCTGTCA	ACACCCGGGA	TGAACTCACC	AGGAATGACG	CCGCCCTTGA	350
TGTCGTTGAC	GAATTCTGTAG	GCTTTGCCTT	CTTCCAGCGG	GTACATGTCG	400
ATCACAAACGT	GACCGTACTG	ACCACGACCA	CCGGACTGCT	TGGCGTGCTT	450
ACCTTCGATA	TCCTTGACGG	TGTTACGAAT	GGTTTCACGG	TAGGCAACCT	500
GC GGCTTACC	TACGTTCGCT	TCTACCTTGA	ACTCGCGACG	CATA CGGTCA	550
ACGATGATGT	CCAGGTGCGAG	CTCACCCATA	CCGGCGATGA	TGGTTTGGCC	600
AGACTCTTCG	TCAGTCCATA	CGCGGAAGGA	CGGGTCTTCC	TGAGGCCAGAC	650
GGCCCAGAGC	CAGGCCATC	TTCTCTTGGT	CAGCCTTGGT	TTTCGGCTCA	700
ACTGCGATGG	AGATTACCGG	TTCCGGGAAT	TCCATACGCT	CGAGGGATGAT	750
CGGCGCTTT	TCGTCACACA	GGGTGTCACC	GGTGGTCACG	TCTTTCAGAC	800
CAATGGCGGC	AGCGATGTCG	CCTGCGCGAA	CTTCTTTGAT	CTCTTCACGC	850

TTGTTGGCGT	GCATCTGAAC	GATACGGCCA	AAACGCTCGC	GCTTCTCTTT	900
AACGGAGTTC	AGCACGGAGT	CACCGGAGTT	AACCACACCG	GAGTAACCGC	950
GGAAGAAGGT	CAGGTTGCCT	ACGAACGGGT	CGGTAGCAAT	CTTGAATGCC	1000
AGAGCAGCAA	ACGGCTCGTC	ATCAGAACGCA	TGACGCTCGT	CTTTGGTCTC	1050
GCCATCCAGC	TTCAGACCGT	CGATGGCTGC	TACGTCGGTC	GGCGCCGGCA	1100
GATAGTCAAC	CACGGCATCC	AGCATGGCCT	GTACGCCCTT	GTTCTTGAAC	1150
GCGGAGCCAC	AGGTAAACAG	GATGATTCG	TTGTTCAGAA	CACGCTGACG	1200
AAGAGCTTTC	TTGATCTCTT	CCTCGGTCA	TTCTTCACCA	CCCAGGTATT	1250
TTTCCATCAG	GTCTTCAGAC	GCTTCAGCAG	CGGCTTCAAC	CAGGGTCATG	1300
CGCATTTCTT	GCGCTTTTC	CAGCAGCTCA	GCCGGGACGT	CTTCGTAATC	1350
GAAGGATACG	CCCTGGTCAG	CTTCGCTCCA	GTTGATGGCT	TTCATCTTGA	1400
CCAGGTCGAT	AACGCCCTTG	AAGTTCTCTT	CTGAACCGAT	GTTCAGTTGC	1450
AGCGGAACCG	GGTTACCTT	CAGACGGTC	TTGATGTGCT	CAACGAGCG	1500
CAGGAAGTTG	GCACCGGTAC	GGTCCATCTT	GTTGACGAAC	GCGATACGGG	1550
GAACCTTGTA	CTTGTAGCC	TGACGCCATA	CGGTTTCAGA	CTGTGGCTGT	1600
ACGCCACHTA	CGGCACAGTA	CACCATCACG	GCGCCGTCCA	GAACACGCAT	1650
GGAACCG					1656

2) INFORMATION FOR SEQ ID NO: 2235

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 155 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Abiotrophia adiacens*
  - (B) STRAIN: ATCC 49175
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

TCTCCTCCCC ATTTGATAAC TACCAAATGA ACGCTATCGA CTGGTTATGT 50  
CAGTCATAAC CAGTTGATTT TTAAGAGAGT TCTTTGGTAT AATTACAATC 100  
GGTAGATACT GTTATAGAAT CTAACAAAAC TCAATTATA GGAGGAATCA 150  
TTTAA 155

2) INFORMATION FOR SEQ ID NO: 2236

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Acinetobacter baumannii*
  - (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236

TCTTTCGATT ACTATAAGCC CTAACATAATT CTTAGTTAAA AACCAAGTGC	50
TCATGGAGCG ACCCTCCATG AGTAGTTAAT AAAGGAAGAT CATC	94

## 2) INFORMATION FOR SEQ ID NO: 2237

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237

GTCCCCACCGG GGGTGAGTGG GGGCCGGGCA ATCGGCCCT GCGAGCCGCC	50
TCACACACCA GTAATCCCAG TAGGTCTCAT GCCCCATGGG TGTAAAGTG	100
ACACCTAGCC GTAGGCTGAG AATTCTACC CGAGTCCAGG AGGACGAAAA	150

## 2) INFORMATION FOR SEQ ID NO: 2238

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238

TTCAGTCCTT TAGGCAAGGA GTTAATTGTC

30

## 2) INFORMATION FOR SEQ ID NO: 2239

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2239

CAACTAGCCT CTCGCTTATC TCCCTATGCA AAATTTCTAG TCAGTTACAG	50
GGCATAGGGG GAGCGTAGGC GGGGGTAGCG GCTTGCTGAG CACTTCCTCT	100
ACATCAAAGG GAATGTTGAG CCGGCCGTTA CCCTGTACGA TCCCACATCTGG	150
TTTCTTCGGT GGTTTGATAA ATACCCCGTT GTGACCCCTAG GATCATGTAA	200
CTGGCACAAAT GTAAATAGCT GTACTGCCAG GCTGCCGAAT TAGCAGTCAG	250
AAATGTACAG CACTGTCAAC TCGTGGCTGC GAAATCGTAG CCACCAACGAA	300
GTCCAGGAGG ACACACA	317

2) INFORMATION FOR SEQ ID NO: 2240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterobacter cloacae*
- (B) STRAIN: ATCC 13047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240

TCCACAGGAT TAAAACCTAA GTCCCGTGCT CTCTCCTGAG GGGAGAGCAC	50
TATAGTAAGG AATATAGCC	69

2) INFORMATION FOR SEQ ID NO: 2241

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*
- (B) STRAIN: ATCC 13883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241

TCCACAGGAT TAAAACCTAA GTCCCGTGCT CTCTCCGAAG GGGAGAGCAC	50
TATAGTAAGG AATATAGCC	69

## 2) INFORMATION FOR SEQ ID NO: 2242

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Listeria monocytogenes*
- (B) STRAIN: ATCC 15313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242

AACAAACAAAG AAGATTAATT GATTTTTTTC GCAACATCAA GTATAACTTT	50
AGTTAGAAAGT ATTACTTAGT TTAAATTAA GCTAAGTAAA AAATAATTAT	100
CGAATTATCG AGGAGGATAT TTTAAA	126

## 2) INFORMATION FOR SEQ ID NO: 2243

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium avium*
- (B) STRAIN: ATCC 25291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2243

GTGTCAACTC ACTGGCTCGG AGCCGAGCAA TCGGCTCAGC GAAGGCGACG	50
GGTCAGTAGC TACTGGCAGC GGAGTAATCT TGCCGGGTCA TTGGAATGCC	100
TTGGGCGCGG CACAACTGAA AACACCAACA CTGCTTTAAC AAGCACCAAC	150
TAGTCCAGGA GGACACAGAA	170

## 2) INFORMATION FOR SEQ ID NO: 2244

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

1153

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium gordoneae*
- (B) STRAIN: Mgor-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244

GGCCGGCAAG CCTGCGAGTA AGCTGACGCG GTTAGCACCG CGGCAAAACC AAGAAAAATC AACACTGCTT TTTTAAGCAC CAACAGTCCA GGAGGACAAC AAA	50 100 103
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## 2) INFORMATION FOR SEQ ID NO: 2245

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245

GCCGAGCGTT GCGCGTAAGC TAGCTCGTT ACCACGGCGG CAAAACCTAGA AAAACATCAA CACTGCTTT ATAAGCACCA ACAGTCCAGG AGGACACAGA A	50 100 101
--	------------------

## 2) INFORMATION FOR SEQ ID NO: 2246

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246

CCAGCTTCCC GCCCGTGCCG CTACGGTGGC ACAAAACCAA AAAGATCAAT CCTGCTGTAA CCCAGCACCA ACAAGTCCAG GAGGACAAGA A	50 91
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## 2) INFORMATION FOR SEQ ID NO: 2247

1154

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria polysaccharea*
- (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247

TCAGGCAAAT AGGCCGTCTG AAAGGCTGAA ATGATTTTC AGACGGCATT	50
GTTCTTTAAT CGATCTTAA TGAAAGGAA TTAGCTC	87

## 2) INFORMATION FOR SEQ ID NO: 2248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus epidermidis*
- (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248

TATAACTTGT TAAGACTAGC TATGCTAGGT TAAAATACAG GTTGAGCTTA	50
TTTATAAGCT GACATTTTA TGATTTGATT TTTAGGGTA AATGCATTAT	100
AAAAGAATTA TAAATTCTTT TATGCTACAC TCAATCAATT TTCTTCTCAT	150
GATGGTGAGA AACTATCATG AGAGATAAAAT TTGAAATAAC TTTTATTAAG	200
AATAGGAGAG ATTTAATA	218

## 2) INFORMATION FOR SEQ ID NO: 2249

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus haemolyticus*
- (B) STRAIN: ATCC 29970

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249

TTAAACTTGT TTTAGCTAGA ATTTCTAGGT AAAATACAGC GTAAGCTTAT	50
TAATTAAGCT AACATCTTTA TGAATTGATT TTTTACTGAA AATGCATTAT	100
AAATGAATTA TGAATTCTAA CAATCATTAT GTCTCATGAT GGTGAGAAC	150
TATCATGAGA GATAATATTG AAATAACTTT TACTAGAATA GGAGAGATT	200
AATA	204

## 2) INFORMATION FOR SEQ ID NO: 2250

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250

CCGTCGGATG GTGTCGTATA CCGCGGAGTC GCCGACGG

38

## 2) INFORMATION FOR SEQ ID NO: 2251

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2251

CGGAGCCGTT CTCGCTGCGT TACATGCTGG TGGCTCCG

38

## 2) INFORMATION FOR SEQ ID NO: 2252

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252

CCACATACAG TGTCTCTC

18

## 2) INFORMATION FOR SEQ ID NO: 2253

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253

CATTACCCAA CCGAAAGTA

19

## 2) INFORMATION FOR SEQ ID NO: 2254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254

ACCTGAACAG AGAGAAATG

19

## 2) INFORMATION FOR SEQ ID NO: 2255

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Abiotrophia adiacens*
- (B) STRAIN: ATCC 49175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2255

ATGGCAAAAG AAAAATTGAGCGTTCAAAA CCACACGTTAACATTGGTAC	50
AATCGGCCAC GTTGACCAACG GTAAAACAACTTAACGTCTGCTGCTATCACAA	100
CTGTTTAGC TAAGAAAGGT TTGCGCGCAAG CTCAGATTACGGTTCAATC	150
GATAAGCTC CAGAAGAACG CGAACGTGGT ATCACAATCA ACACCTCTCA	200
CGTTGAGTAC GAAACAGACA CTCGTCACTA TGCTCACGTT GACTGCCAG	250
GACACGCGGA CTACGTTAAA AAC	273

1157

## 2) INFORMATION FOR SEQ ID NO: 2256

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Acinetobacter baumannii*
- (B) STRAIN: ATCC 19606

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256

ATGGCTAAAG CCAAGTTGA ACGTAATAAA CCACACGTAACGTGGGTAC	50
AATCGGTAC GTTGACCATG GTAAAACAAAC TTTAACTGCT GCGATTGCAA	100
CAATTGTGC AAAAACTTAC GGCGGTGAAG CGAAAGATTAC TCTACAAATC	150
GACTCAGCAC CTGAAGAAAA AGCACGTGGT ATTACAATTA ATACATCACA	200
CGTAGAATAC GATTCTCAA CTCGTCACTA CGCACACGTT GACTGCCAG	250
GCCACGCCGA CTACGTTAAA AAC	273

## 2) INFORMATION FOR SEQ ID NO: 2257

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Actinomyces meyeri*
- (B) STRAIN: ATCC 35568

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257

GTGGCGAAGG CCAAGTTGA GCGCACCAAG CCGCACGTCA ACATCGGCAC	50
GATTGGTCAC GTTGACACG GCAAGACGAC GCTGACGGCA GCTATCACCA	100
AGGTGCTGCA TGACAAGTAC CCCGAACGTGA ACGAGTTCAC CCCCTTCGAT	150
CAGGTCGACA ACGCTCCGA GGAGCGCGAT CGTGGCATCA CGATCAACGT	200
CTCTCACGTT GAGTACCAAGA CCGAGGGCGCG TCACTACGCG CACGTTGACG	250
CTCCCGGCCA CGCCGACTAC GTCAAGAAC	279

## 2) INFORMATION FOR SEQ ID NO: 2258

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Clostridium difficile*
- (B) STRAIN: ATCC 9689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258

GTGGCTAAAG AAAAATTGAGTCGTTCCCTA CCGCACGTCA ACGTTGGCAC	50
TATCGGTACAGTTGACCATG GTAAAACCACTCTGACTGCT GCTCTGACTC	100
GCGTTGCTCGGAAGTATTCTGTTCCGCAA TCGTTGATTTCGATAAAATC	150
GACAGCGCAC CAGAAGAAAAAGCTCGTGGTATCACCATCAACACCGCGCA	200
CGTTGAATAC AACTCGCTGATCCGTCACTACGTCACGTTGACTGCCAG	250
GTCACGCTGA CTATGTGAAG AAC	273

2) INFORMATION FOR SEQ ID NO: 2259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Corynebacterium diphtheriae*
- (B) STRAIN: ATCC 27010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259

GTGGCAAAGG CTAAGTCGA GCGTACCAAG CCGCACGTCA ACATCGGCAC	50
CATCGGTACAGTTGACCATG GTAAAGACACACCCACCGCT GCTATCACCA	100
AGGTTTGGC AGACGCTTAC CCAGAGCTGA AGGAAGCTTT CGCTTTCGAT	150
GCCATCGATA AGGCACCCGA AGAGAAAGAG CGTGGTATTA CCATCAACAT	200
CTCCCACGTG GAGTACCAAGA CCGAGAAGCG CCACTACGCA CACGTTGACG	250
CTCCAGGTCA CGCTGACTAC ATCAAGAAC	279

2) INFORMATION FOR SEQ ID NO: 2260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Enterobacter cloacae*  
 (B) STRAIN: ATCC 13047

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260

GTGTCTAAAG	AAAAATTGAA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACCTAC	CCTGACTGCT	GCAATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCTG	CTCGTGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCAG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2261

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Klebsiella pneumoniae* subsp. *pneumoniae*  
 (B) STRAIN: ATCC 13883

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261

GTGTCTAAAG	AAAAATTGAA	ACGTACAAAA	CCGCACGTCA	ACGTTGGTAC	50
TATCGGCCAC	GTTGACCATG	GTAAAACCTAC	CCTGACTGCT	GCCATCACTA	100
CCGTTCTGGC	TAAAACCTAC	GGTGGTTCCG	CTCGCGCATT	CGACCAGATC	150
GATAACGCAC	CAGAAGAAAA	AGCTCGTGGT	ATCACCATCA	ACACCTCTCA	200
CGTTGAATAT	GACACCCGA	CTCGCCACTA	CGCACACGTA	GACTGCCAG	250
GTCACGCCGA	CTATGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2262

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Listeria monocytogenes*  
 (B) STRAIN: ATCC 15313

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262

ATGGCAAAAG	AAAAATTGAA	CCGCTCTAAA	CCCCATGTTA	ACATTGGTAC	50
TATTGGACAC	GTTGACCATG	GTAAAACAAAC	TTTAACGCT	GCAATTACAA	100

CTGTACTTGC	TAAAAAAGGC	TATGCTGATG	CACAAGCTTA	TGACCAAATT	150
GATGGTCTC	CAGAAGAAAAG	AGAACGTGGA	ATCACAAATCT	CTACTGCTCA	200
CGTTGAGTAC	CAAACGTGACA	GCCGTCACTA	TGCACACGTT	GAUTGCCAG	250
GACATGCCGA	TTACGTTAAA	AAC			273

## 2) INFORMATION FOR SEQ ID NO: 2263

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 279 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mycobacterium avium*
  - (B) STRAIN: ATCC 25291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2263

GTGGCGAAGG	CGAAGTTCGA	GCGGACGAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCAACG	GCAAGACCAAC	GCTGACCGCG	GCTATCACCA	100
AGGTTCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCCG	CGCGTTCGAC	150
CAGATCGACA	ACGCGCCCGA	GGAGCGTCAG	CGCGGTATCA	CCATCAACAT	200
CTCCCACGTG	GAGTACCAAGA	CCGACAAGCG	GCAC TACGCT	CACGTCGACG	250
CCCCGGGTCA	CGCCGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2264

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 279 bases
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Mycobacterium gordonaiae*
  - (B) STRAIN: Mgor-1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264

GTGGCGAAGG	CGAAGTTCCA	GCGGACCAAG	CCGCACGTCA	ACATCGGGAC	50
CATCGGTAC	GTTGACCAACG	GCAAGACCAAC	TCTGACCGCG	GCTATCACCA	100
AGGTCCTGCA	CGACAAGTAC	CCGGACCTGA	ACGAGTCCAA	GGCGTTCGAC	150
CAGATCGACA	ACGCGCTGA	GGAGCGTCAG	CGCGGTATCA	CGATCAACAT	200
CGCGCACGTG	GAATACCAAGA	CCGAGAAGCG	TCACTACGCG	CACGTCGACG	250
CCCCGGCCA	CGCCGACTAC	ATCAAGAAC			279

## 2) INFORMATION FOR SEQ ID NO: 2265

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium kansasii*
- (B) STRAIN: Mkan-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265

GTGGCGAAGG CGAAGTTCCA GCGGACCAAG CCCCACGTCA ACATCGGGAC	50
CATCGGTAC GTTGACCACG GCAAGACCAAC CCTGACCGCG GCTATCACCA	100
AGGTCTGCA TGACAAGTTC CCGGACCTGA ACGAGTCGAA GGCCTTCGAC	150
CAGATCGACA ACGCTCCTGA GGAGCGCCAG CGCGGTATCA CGATCAACAT	200
CGCGCACGTG GAGTACCAGA CCGAGAAGCG GCACTATGCA CACGTCGACG	250
CGCCGGGCCA CGCCGACTAC ATCAAGAAC	279

## 2) INFORMATION FOR SEQ ID NO: 2266

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium terrae*
- (B) STRAIN: Mter-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266

GTGGCGAAGG CGAAGTTCGA GCGGACGAAG CCGCACGTCA ACATCGGGAC	50
CATCGGTAC GTTGACCACG GCAAGACCAAC GCTGACCGCG GCTATCACCA	100
AGGTTCTGCA CGACAAGTAC CCGGACCTCA ACGAGTCGCG TGCCTTCGAC	150
CAGATCGACA ACGCTCCGA AGAGCGTCAG CGCGGTATCA CCATCAACAT	200
CTCCCACGTG GAGTACCAGA CCGAGAAGCG GCACTACGCC CACGTCGACG	250
CTCCTGGTCA CGCTGACTAC ATCAAGAAC	279

## 2) INFORMATION FOR SEQ ID NO: 2267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Neisseria polysaccharea*  
 (B) STRAIN: ATCC 43768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267

ATGGCTAAGG AAAAATTGCA ACGTAGCAAA CCGCACGTAA ACGTTGGCAC	50
CATCGGTCAC GTTGACCATG GTAAAACAC TCTGACTGCT GCTTTGACTA	100
CTATTTGGC TAAAAAATTC GGCGGTGCTG CAAAAGCTTA CGACCAAATC	150
GACAACGCAC CCGAAGAAAA AGCACGCGGT ATTACCATTA ACACCTCGCA	200
CGTAGAATAC GAAACCGAAA CCCGCCACTA CGCACACGTA GACTGCCGG	250
GTCACGCCGA CTACGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2268

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Staphylococcus epidermidis*  
 (B) STRAIN: ATCC 14990

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268

ATGGCAAAAG AAAAATTGTA TCGCTCAAAA GAACATGCCA ATATTGGTAC	50
TATCGGTCAC GTTGACCATG GTAAAACAAAC TTTAACAGCT GCTATCGCAA	100
CTGTATTAGC TAAAAATGGT GACACTGTTG CACAATCATA CGATATGATT	150
GACAACGCTC CAGAAGAAAA AGAACGTGGT ATTACAATCA ATACTGCACA	200
TATCGAATAC CAAACTGACA AACGTCACTA TGCTCACGTT GACTGCCAG	250
GACACGCTGA CTATGTTAAA AAC	273

2) INFORMATION FOR SEQ ID NO: 2269

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 bases  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Staphylococcus haemolyticus*  
 (B) STRAIN: ATCC 29970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269

ATGGCAAAAG	AAAAATTGATCGCTCAAAA	GAACATGCCA	ATATTGGTAC	50
TATCGGTAC	GTTGACCATG	GTAAAACCTAC	TTAACAGCT	100
CTGTATTAGC	AAAAATGGT	GACACTGTAG	CACAATCATA	150
GACAACGCTC	CAGAAGAAAA	AGAACGTGGT	ATCACAAATCA	200
CATCGAGTAT	CAAACGTACA	AACGTCACTA	TGCTCACGTT	250
GACACGCTGA	CTATGTTAAA	AAC		273

## 2) INFORMATION FOR SEQ ID NO: 2270

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 812 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Aeromonas hydrophila*
- (B) STRAIN: ATCC 7966

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270

CGATCCTGGT	AGTAGCAGCG	ACTGACGGCC	CGATGCCGCA	GACTCGTGAG	50
CACATCCTGC	TGGGTCGTCA	GGTAGGCCTT	CCGTACATCA	TCGTGTTCAT	100
GAACAAGTGT	GACATGGTAG	ATGACGAAGA	GCTGCTGGAA	CTGGTCGAGA	150
TGGAAGTTCG	CGAACTGCTG	TCCGAGTACG	ACTTCCCAGG	TGATGACCTG	200
CCGGTAGTCC	GTGGTTCYGC	ACTGAAAGCG	CTGGAAGGCG	AAGCTCAGTG	250
GGAAGAGAAG	ATCCTGGAAC	TGGCTGGCCA	CCTGGACACC	TACATTCCGG	300
AGCCGGAGCG	TGCCATCGAC	CTGCCGTCC	TGATGCCATT	CGAAGACGTA	350
TTCTCCATCG	CTGGCCGYGG	TACCGTAGTG	ACCGGTCGTG	TAGAGCGCGG	400
TATCGTCAAA	GTTGGTGAAG	AAAGTGGAAAT	CGTKGGTATC	AAAGATAACCA	450
CCAAGACAC	CTGTACCGGC	GTTGAAATGT	TCCGCAAAC	GCTGGACGAA	500
GGTCGTGCAG	GCGAGAACAT	CGGTGCACTG	CTGCGTGGCG	TGAAGCGTGA	550
AGACGTAGAG	CGTGGTCAGG	TACTGGCAA	GCCGGGCACC	ATCAAGCCGC	600
ACACCAAGTT	YGAATCTGAA	GTGTACGTG	TGTCCAAAGA	AGAAGGTGGT	650
CGTCATACCC	CGTTCTTCAA	AGGCTACCGT	CCGCAGTTCT	ACTTCCGTAC	700
TACCGACGTG	ACCGGTACCA	TCGAACTGCC	GGAAGGCGTA	GAGATGGTAA	750
TGCCGGGCGA	CAACATCAAG	ATGGTTGTTA	CCCTGATTGC	GCCGATCGCG	800
ATGGACGACG	GC				812

## 2) INFORMATION FOR SEQ ID NO: 2271

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Bilophila wadsworthia*

(B) STRAIN: ATCC 49260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271

CGACGGTCCC	ATGCCCCAGA	CCCGTGAGCA	CATCCTGCTC	GCCCGTCAGG	50
TCGGCGTGCC	TCACCTCGTC	GTGTTCATGA	ACAAGTGTGA	CCTCGTCGAC	100
GACCCCGAAC	TGCTCGAACT	CGTCGAAATG	GAAGTCCGCG	AACTGCTGAG	150
CTCCTACGGC	TACCCCGGCG	ATGAAATCCC	GGTTGTCCGC	GGTTCCGCTC	200
TGAAGGCTCT	GBAATCCGAT	AGCGCTGATT	CCCCTGACGC	CCAGTGCCTG	250
CTCGAACTGC	TCGCGCGTTG	CGACAGCTAC	TTCCCGGATC	CGGTCCGCGA	300
AACCGACAAG	CCCTTCCTGA	TGCCCATCGA	AGACGTGTTC	TCCATCTCCG	350
GCCGCGGTAC	CGTGGTCACC	GGTCGTGTGG	AACGTGGCAT	CATCAAGGTC	400
GGCGAAGAAG	TCGAAATCGT	GGGTATCCGT	CCCACCGTGA	AGACGACCTG	450
CACCGGGCGTC	GAAATGTTCC	GCAAGCTGCT	CGATCAGGGC	CAGGCCGGCG	500
ACAACATCGG	CGCTCTGCTC	CGCGGCACGA	AGCGTGACGA	AGTGGAACGC	550
GGCCAGGGTC	TCGCGCTCC	CAAGAGCATC	ACGCCCCACA	AGAAGTTCAA	600
GGCTGAAGTG	TACGTTCTGT	CCAAGGAAGA	AGGCGGCCGC	CATAACCCGT	650
TCTTCACCAGG	CTATCGTCCT	CAGTTCTACT	TCCGTACAC	CGACATCACC	700
GGTATCATCG	CTCTTGAAGA	AGGC GTTGAA	ATGGTTATGC	CCGGCGATAA	750
CGCTACCTTT	AATGTCGAGC	TCATTACACCC	CATGCCATG	GAAAAGGGC	799

2) INFORMATION FOR SEQ ID NO: 2272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Brevundimonas diminuta*
- (B) STRAIN: ATCC 11568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272

GATCCTGGTG	TGCTCGGCCG	CTGACGGCCC	GATGCCGCAG	ACCCGCGAGC	50
ACATCCTGCT	GTCGCGTCAG	GTCGGCGTTC	CGGCGCTGGT	GGTGTTCCTG	100
AAACAAGGTCG	ACATGGTCGA	CGACGAGGAR	CTGCTGGAGC	TGGTCGAGAT	150
GGAAAGTGCAC	GAGCTGCTGA	GCTCGTACCA	GTTCGGGGC	GACGACATCC	200
CGGTGGTCAA	GGGCTCGGCC	CTGGCCGGG	TGGAGGATCG	CGACCCGAC	250
ATCGGCGCCG	AGCGCGTTCT	GGAGCTGATG	GCGGCGGTG	ACAGCTACAT	300
CCCGCAGCCG	GAACGTCCGA	TCGACATGCC	GTTCCTGATG	CCGGTGGAAAG	350
ACGTGTTCTC	GATCTCGGGC	CGCGGCCACCG	TGGTGACGGG	TCGCGTCGAG	400
CGCGGGCGTCG	TCAAGGTCTG	TGAAGAAAGTC	GAAATCGTCG	GCATCCGTCC	450
GGTTCAGAAG	ACGACCTGCA	CGGGCGTCGA	AATGTTCCGC	AAGCTGCTGG	500
AYCAGGGTCA	RGCCGGCGAC	AACGTGGCG	TGCTGCTGCG	CGGCACCAAG	550
CGTGAAGACG	TCGAGCGCGG	CCAGGTGCTG	TGCAAGCCGG	GTTCGATCAC	600
CCCGCACACC	AAGTTCGTGG	CTGAAGCCTA	CATCCTGAAC	AAGGAAGAAG	650
GCGGCCGTCA	CACGCCGTTC	TTCACGAACT	ACCGTCCGCA	GTTCTACTTC	700
CGCACGACGG	ACGTGACCGG	CATCGTGCCTC	CTGAAGGAAG	GCGTCGAGAT	750
GATCATGCCG	GGCGACAAACG	CCGAGCTGGA	CGTCGA		786

## 2) INFORMATION FOR SEQ ID NO: 2273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: LSPQ 2583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273

GCTATTATGG	CTGGATTACT	ATCCAATACG	CTATCCAAGA	ATCCCGTAAC	50
GTACCTGCCG	TCAAATCGCT	GGAAGCAGTC	GGATTAGATA	ATTCAATTGAA	100
ATTCCCTCAAT	GGCCTTGGTA	TCAATTATCC	TGAGATGCAT	TATTCTAATG	150
CGATTTCAAG	TAATACAAGC	GAATCTGGTA	ACCAATACGG	AGCAAGTAGC	200
GAAAAAAATGG	CTGCCGCTTA	CGCTGCCTT	GCTAATGGCG	GTACATATTA	250
CAAACCGCAA	TACGTCAACC	GAGTTGTCTT	TAGCGACGGT	ACAGAAAAAG	300
TCTTTTCAAA	TGGCGGATCA	AAAGCCATGA	AAGAGACGAC	AGCCTACATG	350
ATGACAGACA	TGATGAAGAC	CGTTCTTCAG	TCTGGAACTG	GTACCAATGC	400
TGCAATCCCA	GGAGTTTATC	AAGCAGGTAA	AACTGGTACT	TCCAACATATG	450
CAGATGATGA	GCTAGAGAAG	TTGACAAAAC	CTTATTACAG	TTCTAGCATT	500
GTCACACCAAG	ACGAACATT	TGTTGGCTAT	ACTCCACAAAT	ACTCTATGGC	550
TGTTTGACAA					560

## 2) INFORMATION FOR SEQ ID NO: 2274

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 49456

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274

GCTACTTTGG	AAACATTACT	GTCCAATATG	CTCTTCACAA	ATCACGTAAT	50
GTCACAGCCG	TTGAAACTTT	GAATAAGGTC	GGTCTAGATA	AGGCTAAAGC	100
CTTCCTTAAT	GGGCTTGGTA	TTGATTATCC	AAGCATGCAT	TATGCAAACG	150
CCATTTCAAG	TAATACAAC	GAATCCAACA	AAAAATACGG	TGCAAGTAGT	200
GAAAAAAATGG	CTGCTGCCA	CGCTGCTTT	GCTAATGGTG	GTATTTCACCA	250
CAAGCCAATG	TACATCAATA	AAATCGTCTT	TAGCGACGGT	AGTGAGAAAG	300
AATTTCTGA	TGCCGGCACA	CGAGCTATGA	AAGAAACTAC	TGCCTATATG	350
ATGACTGAAA	TGATGAAAAC	AGTCCTAGTA	TACGGTACCG	GACGTGGAGC	400
CTACCTACCA	TGGCTTCCAC	AAGCAGGTAA	GACAGGTACT	TCTAACTATA	450

CTGACGACGA AATTGAAAAG TATATCAAGA ACACTGGCTA CGTAGCCCCA	500
GATGAAATGT TTGTAGGGTA TACTCGTAAA TATGCAATGG CTGTTTGGAC	550
A	551

## 2) INFORMATION FOR SEQ ID NO: 2275

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus mitis*
- (B) STRAIN: ATCC 903

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275

GCTATTATGG CTGGATTACT ATCCAATACG CTATCCAAGA ATCCCGTAAC	50
GTACCAGCCG TCAAATCGCT GGAAGCAGTC GGATTAGATA ATTCAATTGAA	100
GTTCCTCAAT GGCCTTGGTA TTAATTACCC TGAAATGCAT TATTCTAATG	150
CGATTTCAAG TAATACAAGC GAATCTGGTA ACCAATACGG AGCAAGTAGC	200
GAAAAAAATGG CTGCCGCTTA CGCTGCCTT GCTAATGGCG GTACATATTA	250
CAAACCGCAA TACGTCAACC GAGTTGTCTT TAGCGACGGT ACAGAAAAAG	300
TCTTTTCAAA TGGCGGATCA AAAGCCATGA AAGAAACGAC AGCCTACATG	350
ATGACAGACA TGATGAAGAC CGTTCTTCAA TCTGGAACTG GTACCAATGC	400
TGCAATTCCA GGAGTCTATC AAGCAGGTAA AACCGGGACT TCCAACATATG	450
CAGATGATGA ACTAGAGAAG TTGACAAAAC CTTATTACAG TTCTAGCATT	500
GTCACACCCAG ACGAGCTGTT TGTTGGCTAC ACTCCACAGT ACTCTATGGC	550
TGTTTGGACA	560

## 2) INFORMATION FOR SEQ ID NO: 2276

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus oralis*
- (B) STRAIN: ATCC 35037

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276

TTATTTGGAA AATATCACCA TCCAATATGC GCTCCAACAA TCACGGAACG	50
TTACAGCCGT AGAAACCTTG AACAAAGTCG GTTTGGATAG AGCCAAGACC	100
TTCCTGAATG GAATCGGTAT TGACTATCCA GATATGCCT ATGCCAACGC	150
GATTCAAGT AATACGACTG AGTCAAACAA AAAGTACGGA GCAAGTAGTG	200

AGAAAATGGC	TGCTGCTTAC	GCTGCTTTG	CTAACGGTGG	TATCTACCAT	250
AAACCAATGT	ATATCAACAA	AATCGTCTT	AGCGATGGTA	GCTAAAAGA	300
ATACGCTGAT	CCTGGTACTC	GTGCCATGAA	AGAGACGACC	GCCTATATGA	350
TGACAGAAAT	GATGAAGACT	GTCCTGGCAT	ACGGAACGGG	TCGTGGTGCT	400
TATCTCCCTT	GGCTACCTCA	AGCTGGTAAG	ACTGGTACAT	CAAACATAC	450
AGATGATGAA	ATTGAAAAT	ACATCAAAAA	TACTGGTTAT	GTAGCCCCAG	500
ACGAAATGTT	TGTTGGTTAT	ACTCGCAAAT	ATTCAATGGC	TGTWTGGACA	550

## 2) INFORMATION FOR SEQ ID NO: 2277

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 35401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277

GCTCCTATCT	GGATTATGCG	ATGTCGGTCA	TTGTTGGCCG	TGGCCTGCCA	50
GATGTCCGAG	ATGGCCTGAA	GCCGGTACAC	CGTCGCGTAC	TTTACGCCAT	100
GAACGTACTA	GGCAATGACT	GGAACAAAGC	CTATAAAAAAA	TCTGCCCGTG	150
TCGTTGGTGA	CGTAATCGGT	AAATACCATC	CCCATGGTGA	CTCGGCGGTC	200
TATGACACGA	TCGTCCGCAT	GGCGCAGCCA	TTCTCGCTGC	GTTATATGCT	250
GGTAGACGGT	CAGGGTAACT	TCGGTTCTAT	CGACGGCGAC	TCTGCGGCGG	300
CAATGCGTTA	TACGGAAATC	CGTCTGGCGA	AAATTGCCCA	TGAACGTATG	350
GCCGAT					356

## 2) INFORMATION FOR SEQ ID NO: 2278

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 23511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278

CTCTTATCTG	GATTATGCGA	TGTCGGTCAT	TGTTGGCCGC	GCGCTGCCGG	50
ATGTCCGAGA	TGGCCTGAAG	CCGGTACACC	GTTCGCGTACT	TTACGCCATG	100
AACGTATTGG	GCAATGACTG	GAACAAAGCC	TACAAAAAAT	CAGCCCGTGT	150
CGTTGGTGAC	GTGATCGGT	AATACCACCC	GCACGGCGAC	TCCGCGGTAT	200

ATGACACCAT CGTTCGTATG	GCCCAGCCGT TCTCGCTGCG	CTACATGCTG	250
GTGGATGGCC AGGGGAACCTT	CGGTTCAATC GACGGCGACT	CCGCCGCGGC	300
AATGCGTTAT ACGGAAATCC	GTCTGGCGAA AATTGCTCAC	GAACTGA	347

## 2) INFORMATION FOR SEQ ID NO: 2279

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 43886

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279

AGAGCTCCTA TCTGGATTAT	GCGATGTCGG TCATTGTTGG	CCGTGCGCTG	50
CCAGATGTCC GAGATGGCCT	GAAGCCGGTA CACCGTCGCG	TACTTACGC	100
CATGAACGTA CTAGGCAATG	ACTGGAACAA AGCCTATAAA	AAATCTGCC	150
GTGTCGTTGG TGACGTAATC	GGTAAATACC ATCCCCATGG	TGACTCGGCG	200
GTCTATGACA CGATCGTCCG	CATGGCGCAG CCATTCTCGC	TGGTTATAT	250
GCTGGTAGAC GGTCAAGGTA	ACTTCGGTTC TATCGACGGC	GACTCTGCGG	300
CGGCAATGCG TTATACGGAA	ATCCGTCTGG CGAAAATTGC	CCATGAACTG	350
ATGGCCGATC TC			362

## 2) INFORMATION FOR SEQ ID NO: 2280

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Escherichia coli*
- (B) STRAIN: ATCC 25922

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280

CTCCTATCTG GATTATGCGA	TGTCGGTCAT TGTTGGCCGT	GCGCTGCCAG	50
ATGTCCGAGA TGGCCTGAAG	CCGGTACACC GTCGCGTACT	TTACGCCATG	100
AACGTACTAG GCAATGACTG	GAACAAAGCC TATAAAAAT	CTGCCCGTGT	150
CGTTGGTGAC GTAATCGGT	AATACCATCC CCATGGTGAC	TCGGCGGTTT	200
ATGACACGAT CGTCCGTATG	GCGCAGCCAT TCTCGCTGCG	TTACATGCTG	250
GTAGACGGTC AGGGTAACCTT	CGGTTCCATC GACGGCGACT	CTGCGGGCGC	300
AATGCGTTAT ACGGAAATCC	GTCTGGCGAA AATTGCCAT	GAACTGATGG	350
CCGATCTC			358

## 2) INFORMATION FOR SEQ ID NO: 2281

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281

CCCCCAGCTG GGCGGCGGTA TCGATGGGGG

30

## 2) INFORMATION FOR SEQ ID NO: 2282

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2282

AGRRGCIMAR ATGTATGA

18

## 2) INFORMATION FOR SEQ ID NO: 2283

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283

ATITATGAYG GKITTCAAGAG GC

22

## 2) INFORMATION FOR SEQ ID NO: 2284

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

1170

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284

TCTGWGTRAC IGGYTCKGAG A

21

2) INFORMATION FOR SEQ ID NO: 2285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285

CMCCICCWGG TGGWGAWAC

19

2) INFORMATION FOR SEQ ID NO: 2286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286

AGTTGCTGTA TTAGGAAATG

20

2) INFORMATION FOR SEQ ID NO: 2287

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287

TCGAAGTTGC TGTATTAGGA

20

2) INFORMATION FOR SEQ ID NO: 2288

1171

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1240 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288

TAGAAGCTGG	CTCGTTTTT	TATAAATAAG	TTATTCGTTT	ATTTTGTTT	50
TGTGCTAAAA	TATGAGAGTA	AATCACTGAA	CGATTTAGAA	TACAGGAGGA	100
CAATCTTTG	AAGATTACTT	TACTATATGG	CGGACGCAGC	GCAGAGCAGA	150
GCATGAAGTG	TCCATTCTT	CCGCATTTC	AGTTTAAAT	GCCATTATT	200
ATAATTATTA	CCAAGTTCAA	CTCGTATTAA	TTACAAAAGA	AGGACAATGG	250
GTCAAAGGTC	CATTACTAAC	AGAAAAAACCT	GCCAGCAAAG	ATGTCTTGCA	300
TCTTTCATGG	GACCCAAGTG	GACAGACAGA	GGAAGGCTTT	ACAGGAAAAG	350
TGATCAATCC	GGGCGAAATC	AAAGAAGAAG	GAGCCATCGT	TTTCCAGTT	400
TTACATGGGC	CAAACGGGGA	AGATGGAACG	ATCCAAGGCT	TCTTAGAGAC	450
ATTGAATATG	CCTTATGTCG	GCGCAGGCGT	ATTGACCAAGT	GCATGTGCCA	500
TGGATAAAAT	CATGACCAAG	TATATTTAC	AAGCTGCTGG	TGTGCCGCAA	550
GTTCCATTATG	TACCACTACT	TAAGAATCAA	TGGAAAGAAA	ATCCTAAAAAA	600
AGTATTGAT	CAATGTGAAG	GTTCTTGCT	TTATCCGATG	TTTGTCAAAC	650
CGGCGAATAT	GGGTTCTAGT	GTCGGCATT	CAAAAGCAGA	AAACCGAGAA	700
GAGCTGAAA	ATGCTTTAGC	AACAGCCTAT	CAGTATGATT	CTCGAGCAAT	750
CGTTGAACAA	GGAATTGAAG	CGCGCGAAAT	CGAAGTTGCT	GTATTAGGAA	800
ATGAAGACGT	TCGGACGACT	TTGCCTGGTG	AAGTCGTAAA	AGACGTAGCA	850
TTCTATGATT	ATGAAGCAA	ATATATCAAT	AATAAAATCG	AAATGCAGAT	900
TCCAGCCGAA	GTGCCAGAAG	AAGTTTATCA	AAAAGCGCAA	GAGTACGCGA	950
AGTTAGCTTA	CACGATGTTA	GGTGGAAAGCG	GATTGAGCCG	GTGCGATTTC	1000
TTTTGACAA	ATAAAAATGA	ATTATTCCTG	AATGAATTAA	ACTCTATGCC	1050
AGGATTACG	GAGTTCACTA	TGTACCCACT	CTTATGGGAA	AATATGGGCT	1100
TGAAATACGG	TGATTGATT	GAAGAACTGA	TCCAGTTAGG	AATGAATCGA	1150
TACCATCAGC	GTCAATCTT	TTTGAAAAAA	AATGAATAAA	GAGAAATAAA	1200
GAAGAGGCTG	GAGTGATTGC	GTAACCGCGT	TCATTCTAGC		1240

2) INFORMATION FOR SEQ ID NO: 2289

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289

CACCGAAGAA GATGAAAAAA

20

## 2) INFORMATION FOR SEQ ID NO: 2290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290

TGGCACCGAA GAAGATGA

18

## 2) INFORMATION FOR SEQ ID NO: 2291

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291

ATTTTGGCAC CGAAGAAGA

19

## 2) INFORMATION FOR SEQ ID NO: 2292

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292

GAATCGGCAA GACAATATG

19

## 2) INFORMATION FOR SEQ ID NO: 2293

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

1173

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecium*
- (B) STRAIN: BM4147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293

ATGAATAGAA	TAAAAGTTGC	AATACTGTTT	GGGGGTTGCT	CAGAGGAGCA	50
TGACGTATCG	GTAAAATCTG	CAATAGAGAT	AGCCGCTAAC	ATTAATAAAG	100
AAAAATACGA	GCCGTTATAC	ATTGGAATT	CGAAATCTGG	TGTATGGAAA	150
ATGTGCGAAA	AACCTTGCAC	GGAAATGGAA	AACGACAATT	GCTATTCAAC	200
TGTACTCTCG	CCGGATAAAA	AAATGCACGG	ATTACTTGT	AAAAAGAAC	250
ATGAATATGA	AATCAACCAC	GTTGATGTAG	CATTTTCAGC	TTTGCATGGC	300
AAGTCAGGTG	AAGATGGATC	CATACAAGGT	CTGTTTGAAT	TGTCCGGTAT	350
CCCTTTGTA	GGCTGCGATA	TTCAAAGCTC	AGCAATTGT	ATGGACAAAT	400
CGTTGACATA	CATCGTTGCG	AAAAATGCTG	GGATAGCTAC	TCCCGCCTTT	450
TGGGTTATTA	ATAAAGATGA	TAGGCCGGTG	GCAGCTACGT	TTACCTATCC	500
TGTTTTGTT	AAGCCGGCGC	GTTCAGGCTC	ATCCTTCGGT	GTGAAAAAAAG	550
TCAATAGCGC	GGACGAATTG	GAATACGCAA	TTGAATCGGC	AAGACAATAT	600
GACAGCAAAA	TCTTAATTGA	GCAGGCTGTT	TCGGGCTGTG	AGGTCCGGTTG	650
TGCGGTATTG	GGAAACAGTG	CCCGCGTTAGT	TGTTGGCGAG	GTGGACCAAA	700
TCAGGCTGCA	GTACGGAATC	TTTCGTATTC	ATCAGGAAGT	CGAGCCGGAA	750
AAAGGCTCTG	AAAACGCACT	TATAACCCTT	CCCGCAGACC	TTTCAGCAGA	800
GGAGCGAGGA	CGGATACAGG	AAACGGAAA	AAAAATATAT	AAAGCGCTCG	850
GCTGTAGAGG	TCTAGCCCGT	GTGGATATGT	TTTTACAAGA	TAACGGCCGC	900
ATTGTACTGA	ACGAAGTCAA	TACTCTGCC	GGTTTCACGT	CATACAGTCG	950
TTATCCCCGT	ATGATGGCCG	CTGCAGGTAT	TGCACCTCCC	GAACTGATTG	1000
ACCGCTTGAT	CGTATTAGCG	TTAAAGGGGT	GA		1032

2) INFORMATION FOR SEQ ID NO: 2294

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294

AAACGAGGAT GATTTGATTG

20

2) INFORMATION FOR SEQ ID NO: 2295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

1174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295

TTGAGCAAGC GATTCGG

18

2) INFORMATION FOR SEQ ID NO: 2296

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1029 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Enterococcus faecalis*
- (B) STRAIN: V583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296

ATGAATAAAA	TAAAAGTCGC	AATTATCTTC	GGCGGTTGCT	CGGAGGAACA	50
TGATGTGTCG	GTAAAATCCG	CAATAGAAAT	TGCTGCGAAC	ATTAATACTG	100
AAAAATTGCA	TCCGCACTAC	ATCGGAATTA	CAAAAAACGG	CGTATGGAAG	150
CTATGCAAGA	AGCCATGTAC	GGAATGGGAA	GCCGATAGTC	TCCCCGCCAT	200
ATTCTCCCCG	GATAGGAAAA	CGCATGGTCT	GCTTGTCA	AAAGAAAGAG	250
AATACGAAAC	TCGGCGTATT	GACGTGGCTT	TCCCGGTTTT	GCATGGCAAA	300
TGCGGGGAGG	ATGGTGCGAT	ACAGGGTCTG	TTTGAATTGT	CTGGTATCCC	350
CTATGTAGGC	TGCGATATT	AAAGCTCCGC	AGCTTGCA	GACAAATCAC	400
TGGCCTACAT	TCTTACAAAA	AATGCGGGCA	TCGCCGTCCC	CGAATTCAA	450
ATGATTGAAA	AAGGTGACAA	ACCGGAGGCG	AGGACGCTTA	CCTACCCCTGT	500
CTTTGTGAAG	CCGGCACCGT	CAGGTTCGTC	CTTGGCGTA	ACCAAAGTAA	550
ACAGTACGGA	AGAACTAAC	GCTGCGATAG	AAGCAAGCAGG	ACAATATGAT	600
GGAAAAATCT	TAATTGAGCA	AGCGATTTCG	GGCTGTGAGG	TCGGCTGCGC	650
GGTCATGGGA	AACGAGGATG	ATTGATTGT	CGGCGAAGTG	GATCAAATCC	700
GGTTGAGCCA	CGGTATCTTC	CGCATCCATC	AGGAAAACGA	GCCGGAAAAA	750
GGCTCAGAGA	ATGCGATGAT	TATCGTTCCA	GCAGACATTC	CGGTCGAGGA	800
ACGAAATCGG	GTGCAAGAAA	CGGCAAAGAA	AGTATATCGG	GTGCTTGAT	850
GCAGAGGGCT	TGCTCGTGT	GATCTTTTT	TGCAGGAGGA	TGGCGGCATC	900
GTTCTAACG	AGGTCAATAC	CCTGCCCGGT	TTTACATCGT	ACAGCCGCTA	950
TCCACGCATG	GC GGCTGCCG	CAGGAATCAC	GCTTCCCGCA	CTAATTGACA	1000
GCCTGATTAC	ATTGGCGATA	GAGAGGTGA			1029

2) INFORMATION FOR SEQ ID NO: 2297

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

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PCT/CA00/01150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297

TTCAGGAGGG GGATCGC

17

1176

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